



SEQUENCE LISTING

<110> McDonald, John  
Coggins, Braden  
<120> METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND  
OTHER INFLAMMATORY CONDITIONS AND DISORDERS  
<130> 25020-601B  
<140>  
<141>  
<160> 93  
<170> PatentIn Ver. 2.0  
<210> 1  
<211> 5  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> homo sapien - peptide linker for use in conjugates  
<400> 1  
Gly Gly Gly Gly Ser  
1 5  
<210> 2  
<211> 5  
<212> PRT  
<213> Artificial Sequence  
<220>  
<221> REPEAT  
<222> (1)...(5)  
<223> homo sapien - peptide linker for use in conjugates  
<400> 2  
Gly Gly Gly Gly Ser  
1 5  
<210> 3  
<211> 12  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> homo sapien - peptide linker for use in conjugates  
<400> 3  
Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser  
1 5 10  
<210> 4  
<211> 14  
<212> PRT  
<213> Artificial Sequence  
<220>  
<223> homo sapien - peptide linker for use in conjugates  
<400> 4  
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly  
1 5 10

<210> 5  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> homo sapien - peptide linker for use in conjugates

<400> 5  
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr  
1 5 10 15  
Lys Gly

<210> 6  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> homo sapien - peptide linker for use in conjugates

<400> 6  
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly  
1 5 10

<210> 7  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> homo sapien - peptide linker for use in conjugates

<400> 7  
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr  
1 5 10 15  
Lys Gly

<210> 8  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> homo sapien - peptide linker for use in conjugates

<400> 8  
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe  
1 5 10

<210> 9  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> homo sapien - peptide linker for use in conjugates

<400> 9  
Ser Arg Ser Ser Gly  
1 5

<210> 10  
<211> 5  
<212> PRT

<213> Artificial Sequence

<220>

<223> homo sapien - peptide linker for use in conjugates

<400> 10  
 Ser Gly Ser Ser Cys  
 1 5

<210> 11  
 <211> 28  
 <212> PRT  
 <213> diphtheria toxin trypsin sensitive linker

<400> 11  
 Ala Met Gly Arg Ser Gly Gly Gly Cys Ala Gly Asn Arg Val Gly Ser  
 1 5 10 15  
 Ser Leu Ser Cys Gly Gly Leu Asn Leu Gln Ala Met  
 20 25

<210> 12  
 <211> 6  
 <212> PRT  
 <213> homo sapien

<220>

<221> REPEAT

<222> (3)...(3)

<223> repeat unit 2-4 times

<221> REPEAT

<222> (3)...(4)

<223> repeat family 1-11 times

<400> 12  
 Ala Met Gly Ser Ala Met  
 1 5

<210> 13  
 <211> 74  
 <212> PRT  
 <213> homo sapien

<220>

<223> Human Chemokine Polypeptide: Eotaxin

<400> 13  
 Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn Arg  
 1 5 10 15  
 Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser Gly  
 20 25 30  
 Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys Asp  
 35 40 45  
 Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys Tyr  
 50 55 60  
 Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro  
 65 70

<210> 14  
 <211> 77  
 <212> PRT  
 <213> homo sapien

<220>

<223> Human Chemokine Polypeptide: GCP-2

<400> 14  
 Gly Pro Val Ser Ala Val Leu Thr Glu Leu Arg Cys Thr Cys Leu Arg  
 1 5 10 15  
 Val Thr Leu Arg Val Asn Pro Lys Thr Ile Gly Lys Leu Gln Val Phe  
 20 25 30  
 Pro Ala Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser Leu Lys  
 35 40 45  
 Asn Gly Lys Gln Val Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys Lys  
 50 55 60  
 Val Ile Gln Lys Ile Leu Asp Ser Gly Asn Lys Lys Asn  
 65 70 75

<210> 15  
 <211> 127  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: GM-CSF

<400> 15  
 Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val  
 1 5 10 15  
 Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr  
 20 25 30  
 Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe Asp  
 35 40 45  
 Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys Gln  
 50 55 60  
 Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met Met  
 65 70 75 80  
 Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser Cys  
 85 90 95  
 Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp  
 100 105 110  
 Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
 115 120 125

<210> 16  
 <211> 73  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: MGSA/GRO-Alpha

<400> 16  
 Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln  
 1 5 10 15  
 Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser Pro Gly  
 20 25 30  
 Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Arg  
 35 40 45  
 Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile Ile Glu  
 50 55 60  
 Lys Met Leu Asn Ser Asp Lys Ser Asn  
 65 70

<210> 17  
 <211> 73  
 <212> PRT  
 <213> homo sapien

<220>

<223> Human Chemokine Polypeptide: I309

<400> 17

Lys	Ser	Met	Gln	Val	Pro	Phe	Ser	Arg	Cys	Cys	Phe	Ser	Phe	Ala	Glu
1				5					10					15	
Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu	Cys	Tyr	Arg	Asn	Thr	Ser	Ser
			20					25					30		
Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile	Phe	Lys	Leu	Lys	Arg	Gly	Lys	Glu
		35					40					45			
Ala	Cys	Ala	Leu	Asp	Thr	Val	Gly	Trp	Val	Gln	Arg	His	Arg	Lys	Met
	50					55					60				
Leu	Arg	His	Cys	Pro	Ser	Lys	Arg	Lys							
65					70										

<210> 18

<211> 133

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: Interleukin-3 (IL-3)

<400> 18

Ala	Pro	Met	Thr	Gln	Thr	Thr	Pro	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro	Pro	Leu
			20					25					30		
Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp	Ile	Leu
		35					40					45			
Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	Arg	Ala
	50					55					60				
Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	Lys	Asn
65					70					75				80	
Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	His	Pro
				85					90					95	
Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	Leu	Thr
			100					105					110		
Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	Thr	Thr	Leu
		115					120						125		
Ser	Leu	Ala	Ile	Phe											
130															

<210> 19

<211> 77

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: Interleukin-8 (IL-8)

<400> 19

Ala	Val	Leu	Pro	Arg	Ser	Ala	Lys	Glu	Leu	Arg	Cys	Gln	Cys	Ile	Lys
1				5					10					15	
Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe	Ile	Lys	Glu	Leu	Arg	Val
			20					25					30		
Ile	Glu	Ser	Gly	Pro	His	Cys	Ala	Asn	Thr	Glu	Ile	Ile	Val	Lys	Leu
		35					40					45			
Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro	Lys	Glu	Asn	Trp	Val	Gln
	50					55					60				
Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala	Glu	Asn	Ser			
65					70					75					

<210> 20

<211> 76

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: MCP-1

<400> 20

Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val	Thr	Cys	Cys	Tyr	Asn	Phe	Thr
1				5					10					15	
Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu	Ala	Ser	Tyr	Arg	Arg	Ile	Thr
		20						25					30		
Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val	Ile	Phe	Lys	Thr	Ile	Val	Ala
		35					40					45			
Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln	Lys	Trp	Val	Gln	Asp	Ser	Met
	50					55					60				
Asp	His	Leu	Asp	Lys	Gln	Thr	Gln	Thr	Pro	Lys	Thr				
65					70					75					

<210> 21

<211> 76

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: MCP-2

<400> 21

Gln	Pro	Asp	Ser	Val	Ser	Ile	Pro	Ile	Thr	Cys	Cys	Phe	Asn	Val	Ile
1				5					10					15	
Asn	Arg	Lys	Ile	Pro	Ile	Gln	Arg	Leu	Glu	Ser	Tyr	Thr	Arg	Ile	Thr
		20						25					30		
Asn	Ile	Gln	Cys	Pro	Lys	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Arg	Gly
		35					40					45			
Lys	Glu	Val	Cys	Ala	Asp	Pro	Lys	Glu	Arg	Trp	Val	Arg	Asp	Ser	Met
	50					55					60				
Lys	His	Leu	Asp	Gln	Ile	Phe	Gln	Asn	Leu	Lys	Pro				
65					70					75					

<210> 22

<211> 76

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: MCP-3

<400> 22

Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	Ile
1				5					10					15	
Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	Thr
		20						25					30		
Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Asp
		35					40					45			
Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	Met
	50					55					60				
Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu				
65					70					75					

<210> 23

<211> 75

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: MCP-4

<400> 23  
 Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser  
 1 5 10 15  
 Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr  
 20 25 30  
 Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys  
 35 40 45  
 Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys  
 50 55 60  
 His Leu Gly Arg Lys Ala His Thr Leu Lys Thr  
 65 70 75

<210> 24  
 <211> 70  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: MIP-1-Alpha

<400> 24  
 Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr  
 1 5 10 15  
 Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser  
 20 25 30  
 Ser Gln Cys Ser Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg  
 35 40 45  
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser  
 50 55 60  
 Asp Leu Glu Leu Ser Ala  
 65 70

<210> 25  
 <211> 129  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: Interleukin-4 (IL-4)

<400> 25  
 His Lys Cys Asp Ile Thr Leu Gln Glu Ile Ile Lys Thr Leu Asn Ser  
 1 5 10 15  
 Leu Thr Glu Gln Lys Thr Leu Cys Thr Glu Leu Thr Val Thr Asp Ile  
 20 25 30  
 Phe Ala Ala Ser Lys Asn Thr Thr Glu Lys Glu Thr Phe Cys Arg Ala  
 35 40 45  
 Ala Thr Val Leu Arg Gln Phe Tyr Ser His His Glu Lys Asp Thr Arg  
 50 55 60  
 Cys Leu Gly Ala Thr Ala Gln Gln Phe His Arg His Lys Gln Leu Ile  
 65 70 75 80  
 Arg Phe Leu Lys Arg Leu Asp Arg Asn Leu Trp Gly Leu Ala Gly Leu  
 85 90 95  
 Asn Ser Cys Pro Val Lys Glu Ala Asn Gln Ser Thr Leu Glu Asn Phe  
 100 105 110  
 Leu Glu Arg Leu Lys Thr Ile Met Arg Glu Lys Tyr Ser Lys Cys Ser  
 115 120 125  
 Ser

<210> 26  
 <211> 73  
 <212> PRT  
 <213> homo sapien

<220>

<223> Human Chemokine Poypeptide: MGSA/GRO-Beta

<400> 26

Ala	Pro	Leu	Ala	Thr	Glu	Leu	Arg	Cys	Gln	Cys	Leu	Gln	Thr	Leu	Gln
1				5					10					15	
Gly	Ile	His	Leu	Lys	Asn	Ile	Gln	Ser	Val	Lys	Val	Lys	Ser	Pro	Gly
			20					25					30		
Pro	His	Cys	Ala	Gln	Thr	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asn	Gly	Gln
		35				40					45				
Lys	Ala	Cys	Leu	Asn	Pro	Ala	Ser	Pro	Met	Val	Lys	Lys	Ile	Ile	Glu
	50					55					60				
Lys	Met	Leu	Lys	Asn	Gly	Lys	Ser	Asn							
65					70										

<210> 27

<211> 73

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: MGSA/GRO-gamma

<400> 27

Ala	Ser	Val	Val	Thr	Glu	Leu	Arg	Cys	Gln	Cys	Leu	Gln	Thr	Leu	Gln
1				5					10					15	
Gly	Ile	His	Leu	Lys	Asn	Ile	Gln	Ser	Val	Asn	Val	Arg	Ser	Pro	Gly
			20					25				30			
Pro	His	Cys	Ala	Gln	Thr	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asn	Gly	Lys
		35				40					45				
Lys	Ala	Cys	Leu	Asn	Pro	Ala	Ser	Pro	Met	Val	Gln	Lys	Ile	Ile	Glu
	50					55					60				
Lys	Ile	Leu	Asn	Lys	Gly	Ser	Thr	Asn							
65					70										

<210> 28

<211> 69

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: PARC (MIP-4)

<400> 28

Ala	Gln	Val	Gly	Thr	Asn	Lys	Glu	Leu	Cys	Cys	Leu	Val	Tyr	Thr	Ser
1				5					10					15	
Trp	Gln	Ile	Pro	Gln	Lys	Phe	Ile	Val	Asp	Tyr	Ser	Glu	Thr	Ser	Pro
			20					25				30			
Gln	Cys	Pro	Lys	Pro	Gly	Val	Ile	Leu	Leu	Thr	Lys	Arg	Gly	Arg	Gln
		35				40					45				
Ile	Cys	Ala	Asp	Pro	Asn	Lys	Lys	Trp	Val	Gln	Lys	Tyr	Ile	Ser	Asp
	50					55					60				
Leu	Lys	Leu	Asn	Ala											
65															

<210> 29

<211> 68

<212> PRT

<213> homo sapien

<220>

<223> Human Chemokine Polypeptide: RANTES

<400> 29

Ser	Pro	Tyr	Ser	Ser	Asp	Thr	Thr	Pro	Cys	Cys	Phe	Ala	Tyr	Ile	Ala
1				5					10					15	
Arg	Pro	Leu	Pro	Arg	Ala	His	Ile	Lys	Glu	Tyr	Phe	Tyr	Thr	Ser	Gly
			20					25					30		



Lys Cys Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln  
                   35                  40                  45  
 Val Cys Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser  
           50                  55                  60  
 Leu Glu Met Ser  
 65

<210> 30  
 <211> 69  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: MIP-1-Beta

<400> 30  
 Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys Phe Ser Tyr Thr  
   1                  5                  10                  15  
 Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr Tyr Glu Thr Ser  
           20                  25                  30  
 Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr Lys Arg Ser Lys  
           35                  40                  45  
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln Glu Tyr Val Tyr  
           50                  55                  60  
 Asp Leu Glu Leu Asn  
 65

<210> 31  
 <211> 323  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: RAP

<400> 31  
 Tyr Ser Arg Glu Lys Asn Gln Pro Lys Pro Ser Pro Lys Arg Glu Ser  
   1                  5                  10                  15  
 Gly Glu Glu Phe Arg Met Glu Lys Leu Asn Gln Leu Trp Glu Lys Ala  
           20                  25                  30  
 Gln Arg Leu His Leu Pro Pro Val Arg Leu Ala Glu Leu His Ala Asp  
           35                  40                  45  
 Leu Lys Ile Gln Glu Arg Asp Glu Leu Ala Trp Lys Lys Leu Lys Leu  
           50                  55                  60  
 Asp Gly Leu Asp Glu Asp Gly Glu Lys Glu Ala Arg Leu Ile Arg Asn  
   65                  70                  75                  80  
 Leu Asn Val Ile Leu Ala Lys Tyr Gly Leu Asp Gly Lys Lys Asp Ala  
           85                  90                  95  
 Arg Gln Val Thr Ser Asn Ser Leu Ser Gly Thr Gln Glu Asp Gly Leu  
           100                  105                  110  
 Asp Asp Pro Arg Leu Glu Lys Leu Trp His Lys Ala Lys Thr Ser Gly  
           115                  120                  125  
 Lys Phe Ser Gly Glu Glu Leu Asp Lys Leu Trp Arg Glu Phe Leu His  
           130                  135                  140  
 His Lys Glu Lys Val His Glu Tyr Asn Val Leu Glu Thr Leu Ser  
   145                  150                  155                  160  
 Arg Thr Glu Glu Ile His Glu Asn Val Ile Ser Pro Ser Asp Leu Ser  
           165                  170                  175  
 Asp Ile Lys Gly Ser Val Leu His Ser Arg His Thr Glu Leu Lys Glu  
           180                  185                  190  
 Lys Leu Arg Ser Ile Asn Gln Gly Leu Asp Arg Leu Arg Arg Val Ser  
           195                  200                  205  
 His Gln Gly Tyr Ser Thr Glu Ala Glu Phe Glu Glu Pro Arg Val Ile  
           210                  215                  220  
 Asp Leu Trp Asp Leu Ala Gln Ser Ala Asn Leu Thr Asp Lys Glu Leu

225					230					235				240
Glu	Ala	Phe	Arg	Glu	Glu	Leu	Lys	His	Phe	Glu	Ala	Lys	Ile	Glu
				245					250					255
His	Asn	His	Tyr	Gln	Lys	Gln	Leu	Glu	Ile	Ala	His	Glu	Lys	Leu
			260					265					270	
His	Ala	Glu	Ser	Val	Gly	Asp	Gly	Glu	Arg	Val	Ser	Arg	Ser	Arg
		275					280				285			
Lys	His	Ala	Leu	Leu	Glu	Gly	Arg	Thr	Lys	Glu	Leu	Gly	Tyr	Thr
	290				295					300				
Lys	Lys	His	Leu	Gln	Asp	Leu	Ser	Gly	Arg	Ile	Ser	Arg	Ala	Arg
305				310					315					320
Asn	Glu	Leu												

<210> 32  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Human Chemokine Polypeptide: Stromal cell-derived  
 Factor-1-Alpha (SDF-1-Alpha)

<300>  
 <303> Genomics  
 <304> 28  
 <306> 495-500  
 <307> 1995

<400> 32														
Met	Asn	Ala	Lys	Val	Val	Val	Val	Leu	Val	Leu	Val	Leu	Thr	Ala
1				5					10					15
Cys	Leu	Ser	Asp	Gly	Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro
			20					25					30	Cys
Arg	Phe	Phe	Glu	Ser	His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu
		35					40					45		Lys
Ile	Leu	Asn	Thr	Pro	Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu
	50				55					60				Lys
Asn	Asn	Asn	Arg	Gln	Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile
65				70					75					80
Glu	Tyr	Leu	Glu	Lys	Ala	Leu	Asn	Lys						
				85										

<210> 33  
 <211> 71  
 <212> PRT  
 <213> homo sapien

<220>  
 <223> Human Chemokine Polypeptide: TARC

<400> 33														
Ala	Arg	Gly	Thr	Asn	Val	Gly	Arg	Glu	Cys	Cys	Leu	Glu	Tyr	Phe
1				5					10					15
Gly	Ala	Ile	Pro	Leu	Arg	Lys	Leu	Lys	Thr	Trp	Tyr	Gln	Thr	Ser
			20					25					30	Glu
Asp	Cys	Ser	Arg	Asp	Ala	Ile	Val	Phe	Val	Thr	Val	Gln	Gly	Arg
		35					40					45		Ala
Ile	Cys	Ser	Asp	Pro	Asn	Asn	Lys	Arg	Val	Lys	Asn	Ala	Val	Lys
	50				55						60			Tyr
Leu	Gln	Ser	Leu	Glu	Arg	Ser								
65					70									

<210> 34  
 <211> 247

<212> PRT  
 <213> Bryonia dioica

<400> 34  
 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val  
 1 5 10 15  
 Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val Tyr  
 20 25 30  
 Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Ser Gly Arg Tyr Thr  
 35 40 45  
 Leu Leu His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Val  
 50 55 60  
 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val Ser  
 65 70 75 80  
 Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Phe Val Phe  
 85 90 95  
 Lys Asp Ala Lys Lys Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu  
 100 105 110  
 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly  
 115 120 125  
 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Tyr Tyr Thr Ala  
 130 135 140  
 Ser Ser Ala Ala Ser Ala Leu Leu Val Leu Ile Gln Ser Thr Ala Glu  
 145 150 155 160  
 Ser Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp  
 165 170 175  
 Lys Thr Phe Leu Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Asn Trp  
 180 185 190  
 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln  
 195 200 205  
 Phe Glu Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val Ser  
 210 215 220  
 Ile Thr Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu Leu  
 225 230 235 240  
 Leu Asn Arg Asn Asn Ile Ala  
 245

<210> 35  
 <211> 275  
 <212> PRT  
 <213> Saponaria officinalis

<400> 35  
 Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr  
 1 5 10 15  
 Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu  
 20 25 30  
 Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu  
 35 40 45  
 Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu  
 50 55 60  
 Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp  
 65 70 75 80  
 Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser  
 85 90 95  
 Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys  
 100 105 110  
 Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln  
 115 120 125  
 Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp  
 130 135 140  
 Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val  
 145 150 155 160  
 Lys Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu  
 165 170 175  
 Ala Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro  
 180 185 190

Asn	Lys	Phe	Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp
		195					200					205			
Lys	Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe
	210					215					220				
Asn	Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp
225					230					235					240
Leu	Gln	Met	Gly	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys	Ser	Ser	Asn	
				245				250					255		
Glu	Ala	Asn	Ser	Thr	Val	Arg	His	Tyr	Gly	Pro	Leu	Lys	Pro	Thr	Leu
			260					265					270		
Leu	Ile	Thr													
		275													

<210> 36  
 <211> 250  
 <212> PRT  
 <213> Momordica charantia

<400> 36															
Ala	Pro	Thr	Leu	Glu	Thr	Ile	Ala	Ser	Leu	Asp	Leu	Asn	Asn	Pro	Thr
1				5					10					15	
Thr	Tyr	Leu	Ser	Phe	Ile	Thr	Asn	Ile	Arg	Thr	Lys	Val	Ala	Asp	Lys
		20					25						30		
Thr	Glu	Gln	Cys	Thr	Ile	Gln	Lys	Ile	Ser	Lys	Thr	Phe	Thr	Gln	Arg
		35				40						45			
Tyr	Ser	Tyr	Ile	Asp	Leu	Ile	Val	Ser	Ser	Thr	Gln	Lys	Ile	Thr	Leu
50					55						60				
Ala	Ile	Asp	Met	Ala	Asp	Leu	Tyr	Val	Leu	Gly	Tyr	Ser	Asp	Ile	Ala
65				70						75				80	
Asn	Asn	Lys	Gly	Arg	Ala	Phe	Phe	Phe	Lys	Asp	Val	Thr	Glu	Ala	Val
				85					90					95	
Ala	Asn	Asn	Phe	Phe	Pro	Gly	Ala	Thr	Gly	Thr	Asn	Arg	Ile	Lys	Leu
			100				105						110		
Thr	Phe	Thr	Gly	Ser	Tyr	Gly	Asp	Leu	Glu	Lys	Asn	Gly	Gly	Leu	Arg
		115					120					125			
Lys	Asp	Asn	Pro	Leu	Gly	Ile	Phe	Arg	Leu	Glu	Asn	Ser	Ile	Val	Asn
	130					135					140				
Ile	Tyr	Gly	Lys	Ala	Gly	Asp	Val	Lys	Lys	Gln	Ala	Lys	Phe	Phe	Leu
145					150					155					160
Leu	Ala	Ile	Gln	Met	Val	Ser	Glu	Ala	Ala	Arg	Phe	Lys	Tyr	Ile	Ser
				165					170					175	
Asp	Lys	Ile	Pro	Ser	Glu	Lys	Tyr	Glu	Glu	Val	Thr	Val	Asp	Glu	Tyr
		180						185					190		
Met	Thr	Ala	Leu	Glu	Asn	Asn	Trp	Ala	Lys	Leu	Ser	Thr	Ala	Val	Tyr
		195					200						205		
Asn	Ser	Lys	Pro	Ser	Thr	Thr	Thr	Ala	Thr	Lys	Cys	Gln	Leu	Ala	Thr
	210					215					220				
Ser	Pro	Val	Thr	Ile	Ser	Pro	Trp	Ile	Phe	Lys	Thr	Val	Glu	Glu	Ile
225					230					235					240
Lys	Leu	Val	Met	Gly	Leu	Leu	Lys	Ser	Ser						
				245					250						

<210> 37  
 <211> 293  
 <212> PRT  
 <213> Shigella dysenteriae

<400> 37															
Lys	Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser
1				5					10					15	
Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser
			20					25					30		
Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn
		35					40					45			
Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe
50						55					60				
Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly

65	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser
					85					90					95	
	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser
				100					105					110		
	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met
				115				120						125		
	Gln	Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser
				130			135					140				
	His	Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg
145						150					155				160	
	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg
				165						170					175	
	Gly	Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met
				180				185						190		
	Thr	Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser
				195				200					205			
	Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile
				210			215					220				
	Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu
225						230					235				240	
	Asn	Cys	His	His	His	Ala	Ser	Arg	Val	Ala	Arg	Met	Ala	Ser	Asp	Glu
				245						250					255	
	Phe	Pro	Ser	Met	Cys	Pro	Ala	Asp	Gly	Arg	Val	Arg	Gly	Ile	Thr	His
				260				265						270		
	Asn	Lys	Ile	Leu	Trp	Asp	Ser	Ser	Thr	Leu	Gly	Ala	Ile	Leu	Met	Arg
			275				280						285			
	Arg	Thr	Ile	Ser	Ser											
																290

<210> 38  
 <211> 319  
 <212> PRT  
 <213> Escherichia coli

<400> 38

Met	Lys	Cys	Ile	Leu	Phe	Lys	Trp	Val	Leu	Cys	Leu	Leu	Leu	Gly	Phe
1				5					10					15	
	Ser	Ser	Val	Ser	Tyr	Ser	Arg	Glu	Phe	Thr	Ile	Asp	Phe	Ser	Gln
				20				25						30	
	Gln	Ser	Tyr	Val	Ser	Ser	Leu	Asn	Ser	Ile	Arg	Thr	Glu	Ile	Ser
				35				40					45		
	Pro	Leu	Glu	His	Ile	Ser	Gln	Gly	Thr	Thr	Ser	Val	Ser	Val	Ile
				50			55					60			Asn
	His	Thr	Pro	Pro	Gly	Ser	Tyr	Phe	Ala	Val	Asp	Ile	Arg	Gly	Leu
65					70					75					80
	Val	Tyr	Gln	Ala	Arg	Phe	Asp	His	Leu	Arg	Leu	Ile	Ile	Glu	Gln
				85					90					95	
	Asn	Leu	Tyr	Val	Ala	Gly	Phe	Val	Asn	Thr	Ala	Thr	Asn	Thr	Phe
				100					105					110	
	Arg	Phe	Ser	Asp	Phe	Thr	His	Ile	Ser	Val	Pro	Gly	Val	Thr	Thr
				115				120					125		
	Ser	Met	Thr	Thr	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala
				130			135					140			
	Leu	Glu	Arg	Ser	Gly	Met	Gln	Ile	Ser	Arg	His	Ser	Leu	Val	Ser
145						150					155				160
	Tyr	Leu	Ala	Leu	Met	Glu	Phe	Ser	Gly	Asn	Thr	Met	Thr	Arg	Asp
				165						170				175	
	Ser	Arg	Ala	Val	Leu	Arg	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu
				180					185					190	
	Phe	Arg	Gln	Ile	Gln	Arg	Glu	Phe	Arg	Gln	Ala	Leu	Ser	Glu	Thr
				195				200					205		
	Pro	Val	Tyr	Thr	Met	Thr	Pro	Gly	Asp	Val	Asp	Leu	Thr	Leu	Asn
				210			215					220			Trp
	Gly	Arg	Ile	Ser	Asn	Val	Leu	Pro	Glu	Tyr	Arg	Gly	Glu	Asp	Gly
225					230						235				240
	Arg	Val	Gly	Arg	Ile	Ser	Phe	Asn	Asn	Ile	Ser	Ala	Ile	Leu	Gly

Val	Ala	Val	Ile	245	Leu	Asn	Cys	His	His	250	Gln	Gly	Ala	Arg	Ser	255	Val	Arg
			260	Glu	Glu	Ser	Gln	Pro	Glu	265	Cys	Gln	Ile	Thr	Gly	270	Asp	Arg
Ala	Val	Asn	275	Lys	Ile	Asn	280	Thr	Leu	Trp	Glu	Ser	285	Asn	Thr	Ala	Ala	
Pro	Val	Ile	290	Leu	Asn	Arg	295	Lys	Ser	Gln	Phe	Leu	Tyr	300	Thr	Thr	Gly	Lys
Ala	Phe	Leu	305	Asn	Arg	Lys	310	Ser	Gln	Phe	Leu	Tyr	315	Thr	Thr	Gly	Lys	

<210> 39  
 <211> 247  
 <212> PRT  
 <213> Trichosantheus kirilowii

Asp	Val	Ser	Phe	Arg	Leu	Ser	Gly	Ala	Thr	Ser	Ser	Ser	Tyr	Gly	Val
1			5						10					15	
Phe	Ile	Ser	Asn	Leu	Arg	Lys	Ala	Leu	Pro	Asn	Glu	Arg	Lys	Leu	Tyr
			20					25					30		
Asp	Ile	Pro	Leu	Leu	Arg	Ser	Ser	Leu	Pro	Gly	Ser	Gln	Arg	Tyr	Ala
		35					40					45			
Leu	Ile	His	Leu	Thr	Asn	Tyr	Ala	Asp	Glu	Thr	Ile	Ser	Val	Ala	Ile
		50				55					60				
Asp	Val	Thr	Asn	Val	Tyr	Ile	Met	Gly	Tyr	Arg	Ala	Gly	Asp	Thr	Ser
65					70				75					80	
Tyr	Phe	Phe	Asn	Glu	Ala	Ser	Ala	Thr	Glu	Ala	Ala	Lys	Tyr	Val	Phe
			85					90					95		
Lys	Asp	Ala	Met	Arg	Lys	Val	Thr	Leu	Pro	Tyr	Ser	Gly	Asn	Tyr	Glu
			100					105					110		
Arg	Leu	Gln	Thr	Ala	Ala	Gly	Lys	Ile	Arg	Glu	Asn	Ile	Pro	Leu	Gly
		115					120					125			
Leu	Pro	Ala	Leu	Asp	Ser	Ala	Ile	Thr	Thr	Leu	Phe	Tyr	Tyr	Asn	Ala
		130				135					140				
Asn	Ser	Ala	Ala	Ser	Ala	Leu	Met	Val	Leu	Ile	Gln	Ser	Thr	Ser	Glu
145					150					155					160
Ala	Ala	Arg	Tyr	Lys	Phe	Ile	Glu	Gln	Gln	Ile	Gly	Lys	Arg	Val	Asp
				165				170						175	
Lys	Thr	Phe	Leu	Pro	Ser	Leu	Ala	Ile	Ser	Leu	Glu	Asn	Ser	Trp	
			180					185				190			
Ser	Ala	Leu	Ser	Lys	Gln	Ile	Gln	Ile	Ala	Ser	Thr	Asn	Asn	Gly	Gln
		195					200					205			
Phe	Glu	Ser	Pro	Val	Val	Leu	Ile	Asn	Ala	Gln	Asn	Gln	Arg	Val	Thr
		210				215					220				
Ile	Thr	Asn	Val	Asp	Ala	Gly	Val	Val	Thr	Ser	Asn	Ile	Ala	Leu	Leu
225					230					235					240
Leu	Asn	Arg	Asn	Asn	Met	Ala									
				245											

<210> 40  
 <211> 88  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapien His-Tag leader sequence

<400> 40

aaggagatatacc	atg	ggc	agc	agc	cat	cat	cat	cat	cat	cac	agc	agc		49
	Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser			
	1				5					10				
ggc	ctg	gtg	ccg	cgc	ggc	agc	cat	atg	ctc	gag	gat	ccg		88
Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Leu	Glu	Asp	Pro		
	15				20					25				

<210> 41  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Homo sapien forward primer (Eotaxin)

<400> 41

gggtaatagc atatggggcc agcttctgtc ccaacca

37

<210> 42  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Homo sapien reverse primer (Eotaxin)

<400> 42

cccgaattct ttcacgcgtg gctttggagt tggagatttt tggt

44

<210> 43  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Homo sapien forward primer (MCP-1)

<400> 43  
gggtaatagc atatgcagcc agatgcaatc aatgccccca

39

<210> 44  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Homo sapien reverse primer (MCP-1)

<400> 44

cccgaattct ttcacgcag tcttcggagt ttgggtttct t

41

<210> 45  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Homo sapien forward primer (MCP-3)

<400> 45  
catatgcaac cggtaggcat caacacg

27

<210> 46  
<211> 33

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Homo sapien reverse primer (MCP-3)  
  
 <400> 46  
 cactagtaac catcgcaagc ttcggggtct gag 33  
  
 <210> 47  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Homo sapien forward primer (SDF-1-Beta)  
  
 <400> 47  
 gggtaatagc atatgaagcc cgtcagcctg agctacag 38  
  
 <210> 48  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Homo sapien reverse primer (SDF-1-Beta)  
  
 <400> 48  
 cccgaattct ttcacgcgcca tcttgaacct cttgtttaaa gctttc 46  
  
 <210> 49  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Shigella dysenteriae forward primer (Shiga)  
  
 <400> 49  
 gggtaatagc atatgaaaga attcaccctg gacttttcc 39  
  
 <210> 50  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Shigella dysenteriae reverse primer (Shiga)  
  
 <400> 50  
 cccggatcca ctagtattaa gcgtgggtg 28  
  
 <210> 51  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Shigella dysenteriae reverse primer (Shiga-His6)  
  
 <400> 51



ccccgatcca ctagtttaat gatgatgggtg gtgggtggcaa ttgag

45

<210> 52  
<211> 978  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (1)..(978)

<220>  
<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP1-AM-truncated Shiga-A1 Subunit

<400> 52  
atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48  
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe  
1 5 10 15  
  
acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96  
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile  
20 25 30  
  
acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144  
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val  
35 40 45  
  
gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192  
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser  
50 55 60  
  
atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg aaa 240  
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys  
65 70 75 80  
  
gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg 288  
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu  
85 90 95  
  
aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc 336  
Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser  
100 105 110  
  
ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg 384  
Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu  
115 120 125  
  
ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat 432  
Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn  
130 135 140  
  
aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt 480  
Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe  
145 150 155 160  
  
gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac 528  
Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His  
165 170 175  
  
gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct 576  
Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser  
180 185 190  
  
tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa 624

Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln		
		195					200					205					
atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	672	
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His		
	210					215					220						
tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	720	
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe		
	225				230					235					240		
gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	768	
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly		
				245					250					255			
ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	816	
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr		
			260					265					270				
gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggc	cgc	ttg	tct	tcc	gtt	864	
Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val		
		275					280					285					
ctg	ccg	gat	tat	cac	ggc	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	912	
Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser		
	290					295					300						
ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	960	
Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn		
	305				310				315						320		
tgc	cac	cac	cac	gct	taa											978	
Cys	His	His	His	Ala													
				325													

<210> 53  
 <211> 984  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(984)

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP1-AM-truncated Shiga-A1 Subunit HIS6

<400> 53																
atg	cag	cca	gat	gca	atc	aat	gcc	cca	gtc	acc	tgc	tgt	tat	aac	ttc	48
Met	Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val	Thr	Cys	Cys	Tyr	Asn	Phe	
1				5					10					15		
acc	aat	agg	aag	atc	tca	gtg	cag	agg	ctc	gcg	agc	tat	aga	aga	atc	96
Thr	Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu	Ala	Ser	Tyr	Arg	Arg	Ile	
			20				25						30			
acc	agc	agc	aag	tgt	ccc	aaa	gaa	gct	gtg	atc	ttc	aag	acc	att	gtg	144
Thr	Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val	Ile	Phe	Lys	Thr	Ile	Val	
			35				40					45				
gcc	aag	gag	atc	tgt	gct	gac	ccc	aag	cag	aag	tgg	gtt	cag	gat	tcc	192
Ala	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln	Lys	Trp	Val	Gln	Asp	Ser	
	50					55					60					

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg aaa	240
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys	
65 70 75 80	
gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg	288
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu	
85 90 95	
aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc	336
Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser	
100 105 110	
ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg	384
Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu	
115 120 125	
ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat	432
Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn	
130 135 140	
aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt	480
Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe	
145 150 155 160	
gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac	528
Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His	
165 170 175	
gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct	576
Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser	
180 185 190	
tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa	624
Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln	
195 200 205	
atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat	672
Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His	
210 215 220	
tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc	720
Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe	
225 230 235 240	
gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc	768
Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly	
245 250 255	
ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act	816
Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr	
260 265 270	
gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt	864
Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val	
275 280 285	
ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc	912
Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser	
290 295 300	
ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat	960
Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn	
305 310 315 320	
tgc cac cac cac cat cat cat taa	984
Cys His His His His His His	
325	

<210> 54  
 <211> 999  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(999)

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP1-AM-SAPORIN

```

<400> 54
atg cag cca gat gca atc aat gcc cca gtc acc tgc tgt tat aac ttc 48
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
  1             5             10             15

acc aat agg aag atc tca gtg cag agg ctc gcg agc tat aga aga atc 96
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
             20             25             30

acc agc agc aag tgt ccc aaa gaa gct gtg atc ttc aag acc att gtg 144
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
             35             40             45

gcc aag gag atc tgt gct gac ccc aag cag aag tgg gtt cag gat tcc 192
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
             50             55             60

atg gac cac ctg gac aag caa acc caa act ccg aag act gcg atg gtt 240
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Val
             65             70             75             80

act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc 288
Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser
             85             90             95

agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa 336
Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys
             100            105            110

tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa gaa aag 384
Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys
             115            120            125

ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct ctg ggc 432
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly
             130            135            140

ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg gat aat 480
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn
             145            150            155            160

acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg agc gcg 528
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala
             165            170            175

gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa aaa gca 576
Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala
             180            185            190

ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg cag atc 624
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile

```

195	200	205	
acc cag ggc gat caa tcc cgc	aaa gaa ctg ggt ctg ggt att gat ctg	672	
Thr Gln Gly Asp Gln Ser Arg	Lys Glu Leu Gly Leu Gly Ile Asp Leu		
210	215 220		
ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa	720		
Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys			
225	230 235 240		
gac gaa gcc cgc ttc ctg ctg atc gcc att cag atg acg gca gaa gcc	768		
Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala			
245	250 255		
gcc cgt ttc cgc tac att cag aac ctg gtc atc aaa aac ttc ccg aac	816		
Ala Arg Phe Phe Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn			
260	265 270		
aag ttc aat tcc gag aat aaa gtc att cag ttc gag gtt aat tgg aaa	864		
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys			
275	280 285		
aaa att tcc acc gcc att tat ggt gac gcg aag aac ggt gtt ttc aat	912		
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn			
290	295 300		
aaa gat tat gat ttt ggt ttc ggt aag gta cgt cag gtg aaa gac ctg	960		
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu			
305	310 315 320		
caa atg ggt ctg ctg atg tac cta gga aaa ccg aag taa	999		
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys			
325	330		

<210> 55  
 <211> 978  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(978)

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 Subunit

<400> 55	
atg caa ccg gta ggc atc aac acg tcg acc acg tgc tgt tat cgc ttt	48
Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe	
1	5 10 15
atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc	96
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr	
20	25 30
act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctc	144
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu	
35	40 45
gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt	192
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe	
50	55 60

atg Met 65	aaa Lys	cat His	ctg Leu	gat Asp	aag Lys 70	aaa Lys	act Thr	cag Gln	acc Thr	ccg Pro 75	aag Lys	ctt Leu	gcg Ala	atg Met	aaa Lys 80	240
gaa Glu	ttc Phe	acc Thr	ctg Leu	gac Asp 85	ttt Phe	tcc Ser	act Thr	gca Ala	aaa Lys 90	act Thr	tac Tyr	gtc Val	gat Asp	agc Ser 95	ctg Leu	288
aat Asn	gtg Val	att Ile	cgt Arg 100	tcc Ser	gcg Ala	atc Ile	ggg Gly	acg Thr 105	ccg Pro	ctg Leu	caa Gln	acg Thr	att Ile 110	tcc Ser	agc Ser	336
ggg Gly	ggg Gly	act Thr 115	tcc Ser	ctc Leu	ctg Leu	atg Met	att Ile 120	gat Asp	tcc Ser	ggg Gly	acg Thr 125	ggg Gly	gat Asp	aac Asn	ttg Leu	384
ttt Phe 130	gct Ala	gtt Val	gat Asp	gtg Val	cgc Arg	ggc Gly 135	att Ile	gac Asp	ccg Pro	gaa Glu	gaa Glu 140	ggc Gly	cgt Arg	ttt Phe	aat Asn	432
aat Asn 145	ctg Leu	cgt Arg	ctg Leu	atc Ile	gtc Val 150	gaa Glu	cgc Arg	aac Asn	aac Asn	ctg Leu 155	tat Tyr	gtg Val	acg Thr	ggg Gly	ttt Phe 160	480
gtg Val	aac Asn	cgt Arg	acg Thr	aac Asn 165	aac Asn	gtc Val	ttc Phe	tat Tyr	cgt Arg 170	ttc Phe	gct Ala	gat Asp	ttc Phe	tcc Ser 175	cac His	528
gta Val	acg Thr	ttt Phe	ccg Pro 180	ggc Gly	acc Thr	act Thr	gct Ala	gtt Val 185	act Thr	ctg Leu	agc Ser	ggc Gly	gat Asp 190	tct Ser	tct Ser	576
tat Tyr	act Thr	acg Thr 195	tta Leu	cag Gln	cgt Arg	gtg Val	gct Ala 200	ggg Gly	atc Ile	agc Ser	cgc Arg	act Thr 205	ggg Gly	atg Met	caa Gln	624
atc Ile 210	aat Asn	cgc Arg	cat His	tct Ser	ctg Leu 215	acg Thr	acc Thr	agc Ser	tat Tyr	ctg Leu 220	gac Asp	tta Leu	atg Met	agc Ser	cat His	672
tct Ser 225	ggc Gly	acc Thr	agc Ser	ctg Leu	acc Thr 230	cag Gln	tct Ser	gtt Val	gcc Ala	cgt Arg 235	gcg Ala	atg Met	ctg Leu	cgc Arg	ttc Phe 240	720
gtg Val	acg Thr	gtc Val	acc Thr	gcc Ala 245	gaa Glu	gcc Ala	ctg Leu	cgt Arg	ttc Phe 250	cgt Arg	caa Gln	atc Ile	caa Gln	cgc Arg 255	ggc Gly	768
ttc Phe	cgc Arg	acc Thr	act Thr 260	tta Leu	gac Asp	gat Asp	ctg Leu	tct Ser 265	ggc Gly	cgc Arg	agc Ser	tat Tyr	gtg Val 270	atg Met	act Thr	816
gcc Ala	gaa Glu	gat Asp 275	gtc Val	gat Asp	ctg Leu	acc Thr	ctg Leu 280	aac Asn	tgg Trp	ggg Gly	cgc Arg	ttg Leu 285	tct Ser	tcc Ser	gtt Val	864
ctg Leu 290	ccg Pro	gat Asp	tat Tyr	cac His	ggg Gly	cag Gln 295	gat Asp	tct Ser	gtc Val	cgt Arg	gtt Val 300	ggc Gly	cgt Arg	atc Ile	agc Ser	912
ttt Phe 305	ggc Gly	tct Ser	att Ile	aat Asn	gcc Ala 310	atc Ile	cta Leu	ggc Gly	tcc Ser	gtc Val 315	gca Ala	ctg Leu	att Ile	ctc Leu	aat Asn 320	960
tgc Cys	cac His	cac His	cac His	gct Ala 325	taa											978

<210> 56  
 <211> 984  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(984)

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein MCP3-AM-truncated Shiga-A1 subunit HIS6

<400> 56  
 atg caa ccg gta ggc atc aac acg tcg acc acg tgc tgt tat cgc ttt 48  
 Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe  
 1 5 10 15  
 atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc 96  
 Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr  
 20 25 30  
 act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctg 144  
 Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu  
 35 40 45  
 gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt 192  
 Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe  
 50 55 60  
 atg aaa cat ctg gat aag aaa act cag acc ccg aag ctt gcg atg aaa 240  
 Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu Ala Met Lys  
 65 70 75 80  
 gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg 288  
 Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu  
 85 90 95  
 aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc 336  
 Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser  
 100 105 110  
 ggt ggt act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg 384  
 Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu  
 115 120 125  
 ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat 432  
 Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn  
 130 135 140  
 aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt 480  
 Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe  
 145 150 155 160  
 gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac 528  
 Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His  
 165 170 175  
 gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct 576  
 Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser  
 180 185 190  
 tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa 624  
 Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln  
 195 200 205

atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat	672
Ile Asn Arg His Ser Leu Thr Ser Tyr Leu Asp Leu Met Ser His	
210 215 220	
tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc	720
Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe	
225 230 235 240	
gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc	768
Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly	
245 250 255	
ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act	816
Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr	
260 265 270	
gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt	864
Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val	
275 280 285	
ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc	912
Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser	
290 295 300	
ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat	960
Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn	
305 310 315 320	
tgc cac cac cac cat cat cat taa	984
Cys His His His His His His	
325	

<210> 57

<211> 999

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(999)

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin Fusion Protein MCP3-AM-SAPORIN

<400> 57

atg caa ccg gta ggc atc aac acg tcc acc acg tgc tgt tat cgc ttt	48
Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe	
1 5 10 15	
atc aac aag aaa atc ccg aaa caa cgc ctg gaa tcc tat cgt cgc acc	96
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr	
20 25 30	
act agc agc cac tgt ccg cgc gaa gca gtc atc ttc aaa acc aag ctc	144
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu	
35 40 45	
gat aag gaa atc tgt gca gac ccg act cag aaa tgg gtg caa gat ttt	192
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe	
50 55 60	
atg aaa cat ctg gat aag aaa act cag acc ccg aag ctt gcg atg gtt	240
Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu Ala Met Val	
65 70 75 80	



act	agt	att	acc	ctg	gac	ctg	gtc	aat	ccg	acc	gcc	ggc	caa	tat	agc	288
Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	
				85					90					95		
agc	ttc	gtg	gat	aag	att	cgt	aac	aac	gta	aaa	gat	ccg	aat	ctg	aaa	336
Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	
			100				105						110			
tac	ggg	ggg	act	gat	att	gcg	gtc	atc	ggg	ccg	ccg	agc	aaa	gaa	aag	384
Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	
		115					120					125				
ttc	ctg	cgc	att	aac	ttt	caa	agc	tcc	cgt	ggc	act	gtt	tct	ctg	ggc	432
Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	
	130					135					140					
ctg	aag	cgc	gat	aac	ctg	tat	gtt	gtt	gcc	tat	ctg	gcg	atg	gat	aat	480
Leu	Lys	Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	
145					150					155					160	
acg	aac	gtg	aac	cgc	gcc	tac	tac	ttt	cgt	agc	gag	att	acg	agc	gcg	528
Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr	Ser	Ala	
				165					170					175		
gaa	tcc	act	gct	ctg	ttc	ccg	gag	gcg	acc	act	gca	aac	caa	aaa	gca	576
Glu	Ser	Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	
			180					185					190			
ctg	gaa	tat	acg	gaa	gat	tac	cag	tcc	atc	gag	aag	aac	gcg	cag	atc	624
Leu	Glu	Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala	Gln	Ile	
		195					200					205				
acc	cag	ggc	gat	caa	tcc	cgc	aaa	gaa	ctg	ggg	ctg	ggg	att	gat	ctg	672
Thr	Gln	Gly	Asp	Gln	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile	Asp	Leu	
	210					215					220					
ctg	agc	acg	agc	atg	gaa	gcg	gtc	aac	aaa	aaa	gct	cgc	gtg	gtt	aaa	720
Leu	Ser	Thr	Ser	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val	Val	Lys	
225					230				235						240	
gac	gaa	gcc	cgc	ttc	ctg	ctg	atc	gcc	att	cag	atg	acg	gca	gaa	gcc	768
Asp	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Ala	
				245				250					255			
gcc	cgt	ttc	cgc	tac	att	cag	aac	ctg	gtc	atc	aaa	aac	ttc	ccg	aac	816
Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	Pro	Asn	
			260				265						270			
aag	ttc	aat	tcc	gag	aat	aaa	gtc	att	cag	ttc	gag	gtt	aat	tgg	aaa	864
Lys	Phe	Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp	Lys	
		275					280					285				
aaa	att	tcc	acc	gcc	att	tat	ggg	gac	gcg	aag	aac	ggg	gtt	ttc	aat	912
Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	
		290				295					300					
aaa	gat	tat	gat	ttt	ggg	ttc	ggg	aag	gta	cgt	cag	gtg	aaa	gac	ctg	960
Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	
305					310				315						320	
caa	atg	ggg	ctg	ctg	atg	tac	cta	gga	aaa	ccg	aag	taa				999
Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys					
				325					330							

<210> 58  
<211> 963

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF-1-Beta-AM-truncated Shiga-A1 Subunit

<220>  
 <221> CDS  
 <222> (1)..(963)

```

<400> 58
aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc 48
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
1 5 10 15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca 96
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
20 25 30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa 144
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
35 40 45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa 192
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
50 55 60

gct tta aac aag agg ttc aag atg gcg atg aaa gaa ttc acc ctg gac 240
Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp
65 70 75 80

ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg att cgt tcc 288
Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser
85 90 95

gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt act tcc ctc 336
Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu
100 105 110

ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct gtt gat gtg 384
Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val
115 120 125

cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg cgt ctg atc 432
Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile
130 135 140

gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac cgt acg aac 480
Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn
145 150 155 160

aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg ttt ccg ggc 528
Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly
165 170 175

acc act gct gtt act ctg agc ggc gat tct tct tat act acg tta cag 576
Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln
180 185 190

cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat cgc cat tct 624
Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser
195 200 205

ctg acg acc agc tat ctg gac tta atg agc cat tct ggc acc agc ctg 672

```

Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	Ser	Gly	Thr	Ser	Leu	
210						215					220					
acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	gtg	acg	gtc	acc	gcc	720
Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	Val	Thr	Val	Thr	Ala	
225					230					235					240	
gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	ttc	cgc	acc	act	tta	768
Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	Phe	Arg	Thr	Thr	Leu	
				245					250					255		
gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	gcc	gaa	gat	gtc	gat	816
Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu	Asp	Val	Asp	
			260					265					270			
ctg	acc	ctg	aac	tgg	ggc	cgc	ttg	tct	tcc	gtt	ctg	ccg	gat	tat	cac	864
Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro	Asp	Tyr	His	
		275					280					285				
ggc	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	ttt	ggc	tct	att	aat	912
Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly	Ser	Ile	Asn	
	290					295					300					
gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	tgc	cac	cac	cac	gct	960
Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His	His	His	Ala	
305					310					315					320	
taa																963

<210> 59

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF-1-Beta-AM-truncated Shiga-A1 Subunit HIS6

<220>

<221> CDS

<222> (1)..(969)

<400> 59

aag	ccc	gtc	agc	ctg	agc	tac	aga	tgc	cca	tgc	cga	ttc	ttc	gaa	agc	48
Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu	Ser	
1				5				10						15		
cat	gtt	gcc	aga	gcc	aac	gtc	aag	cat	ctc	aaa	att	ctc	aac	act	cca	96
His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr	Pro	
			20				25					30				
aac	tgt	gcc	ctt	cag	att	gta	gcc	cgg	ctg	aag	aac	aac	aac	aga	caa	144
Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg	Gln	
		35					40					45				
gtg	tgc	att	gac	ccg	aag	cta	aag	tgg	att	cag	gag	tac	ctg	gag	aaa	192
Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu	Lys	
	50					55					60					
gct	tta	aac	aag	agg	ttc	aag	atg	gcg	atg	aaa	gaa	ttc	acc	ctg	gac	240
Ala	Leu	Asn	Lys	Arg	Phe	Lys	Met	Ala	Met	Lys	Glu	Phe	Thr	Leu	Asp	
65					70					75					80	
ttt	tcc	act	gca	aaa	act	tac	gtc	gat	agc	ctg	aat	gtg	att	cgt	tcc	288

Phe	Ser	Thr	Ala	Lys 85	Thr	Tyr	Val	Asp	Ser 90	Leu	Asn	Val	Ile	Arg 95	Ser	
gcg	atc	ggt	acg	ccg	ctg	caa	acg	att	tcc	agc	ggt	ggt	act	tcc	ctc	336
Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	Thr	Ser	Leu	
			100					105					110			
ctg	atg	att	gat	tcc	ggt	acg	ggt	gat	aac	ttg	ttt	gct	ggt	gat	gtg	384
Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	Phe	Ala	Val	Asp	Val	
		115					120					125				
cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	aat	ctg	cgt	ctg	atc	432
Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	Arg	Leu	Ile	
	130					135					140					
gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggt	ttt	gtg	aac	cgt	acg	aac	480
Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	Arg	Thr	Asn	
	145				150					155					160	
aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	gta	acg	ttt	ccg	ggc	528
Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	Phe	Pro	Gly	
				165					170					175		
acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	tat	act	acg	tta	cag	576
Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln	
			180					185					190			
cgt	gtg	gct	ggt	atc	agc	cgc	act	ggt	atg	caa	atc	aat	cgc	cat	tct	624
Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	Ile	Asn	Arg	His	Ser	
		195					200					205				
ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	tct	ggc	acc	agc	ctg	672
Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	Ser	Gly	Thr	Ser	Leu	
	210					215					220					
acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	gtg	acg	gtc	acc	gcc	720
Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	Val	Thr	Val	Thr	Ala	
	225				230					235					240	
gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	ttc	cgc	acc	act	tta	768
Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	Phe	Arg	Thr	Thr	Leu	
				245					250					255		
gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	gcc	gaa	gat	gtc	gat	816
Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu	Asp	Val	Asp	
			260					265					270			
ctg	acc	ctg	aac	tgg	ggt	cgc	ttg	tct	tcc	gtt	ctg	ccg	gat	tat	cac	864
Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro	Asp	Tyr	His	
		275					280					285				
ggt	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	ttt	ggc	tct	att	aat	912
Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly	Ser	Ile	Asn	
	290					295					300					
gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	tgc	cac	cac	cac	cat	960
Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His	His	His	His	
	305				310					315					320	
cat	cat	taa														969
His	His															

<210> 60  
 <211> 984  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein SDF-1-Beta-AM-SAPORIN

<220>  
 <221> CDS  
 <222> (1)..(984)

```

<400> 60
aag ccc gtc agc ctg agc tac aga tgc cca tgc cga ttc ttc gaa agc   48
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
1          5          10          15

cat gtt gcc aga gcc aac gtc aag cat ctc aaa att ctc aac act cca   96
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
          20          25          30

aac tgt gcc ctt cag att gta gcc cgg ctg aag aac aac aac aga caa   144
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Arg Gln
          35          40          45

gtg tgc att gac ccg aag cta aag tgg att cag gag tac ctg gag aaa   192
Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
          50          55          60

gct tta aac aag agg ttc aag atg gcg atg gtt act agt att acc ctg   240
Ala Leu Asn Lys Arg Phe Lys Met Ala Met Val Thr Ser Ile Thr Leu
          65          70          75

gac ctg gtc aat ccg acc gcc ggc caa tat agc agc ttc gtg gat aag   288
Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys
          85          90          95

att cgt aac aac gta aaa gat ccg aat ctg aaa tac ggt ggt act gat   336
Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp
          100          105          110

att gcg gtc atc ggt ccg ccg agc aaa gaa aag ttc ctg cgc att aac   384
Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn
          115          120          125

ttt caa agc tcc cgt ggc act gtt tct ctg ggc ctg aag cgc gat aac   432
Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn
          130          135          140

ctg tat gtt gtt gcc tat ctg gcg atg gat aat acg aac gtg aac cgc   480
Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg
          145          150          155

gcc tac tac ttt cgt agc gag att acg agc gcg gaa tcc act gct ctg   528
Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser Thr Ala Leu
          165          170          175

ttc ccg gag gcg acc act gca aac caa aaa gca ctg gaa tat acg gaa   576
Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu
          180          185          190

gat tac cag tcc atc gag aag aac gcg cag atc acc cag ggc gat caa   624
Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Gln
          195          200          205

tcc cgc aaa gaa ctg ggt ctg ggt att gat ctg ctg agc acg agc atg   672
Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser Thr Ser Met
          210          215          220

```

gaa gcg gtc aac aaa aaa gct cgc gtg gtt aaa gac gaa gcc cgc ttc	720
Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu Ala Arg Phe	
225 230 235 240	
ctg ctg atc gcc att cag atg acg gca gaa gcc gcc cgt ttc cgc tac	768
Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala Ala Arg Phe Arg Tyr	
245 250 255	
att cag aac ctg gtc atc aaa aac ttc ccg aac aag ttc aat tcc gag	816
Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn Lys Phe Asn Ser Glu	
260 265 270	
aat aaa gtc att cag ttc gag gtt aat tgg aaa aaa att tcc acc gcc	864
Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys Lys Ile Ser Thr Ala	
275 280 285	
att tat ggt gac gcg aag aac ggt gtt ttc aat aaa gat tat gat ttt	912
Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe	
290 295 300	
ggt ttc ggt aag gta cgt cag gtg aaa gac ctg caa atg ggt ctg ctg	960
Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu	
305 310 315 320	
atg tac cta gga aaa ccg aag taa	984
Met Tyr Leu Gly Lys Pro Lys	
325	

<210> 61

<211> 972

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(972)

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit

<400> 61

atg ggg cca gct tct gtc cca acc acc tgc tgc ttt aac ctg gcc aat	48
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn	
1 5 10 15	

agg aag ata ccc ctt cag cga cta gag agc tac agg aga atc acc agt	96
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser	
20 25 30	

ggc aaa tgt ccc cag aaa gct gtg atc ttc aag acc aaa ctg gcc aag	144
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys	
35 40 45	

gat atc tgt gcc gac ccc aag aag aag tgg gtg cag gat tcc atg aag	192
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys	
50 55 60	

tat ctg gac caa aaa tct cca act cca aag cca gcg atg aaa gaa ttc	240
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Lys Glu Phe	
65 70 75 80	

acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg	288
Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val	
85 90 95	

att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	tcc	agc	ggg	ggg	336
Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	
			100					105					110			
act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	aac	ttg	ttt	gct	384
Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	Phe	Ala	
		115					120					125				
gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	ttt	aat	aat	ctg	432
Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	
	130					135					140					
cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	ggg	ttt	gtg	aac	480
Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	
	145					150				155					160	
cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	tcc	cac	gta	acg	528
Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	
				165					170					175		
ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	tct	tct	tat	act	576
Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	
			180					185					190			
acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	atg	caa	atc	aat	624
Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	Ile	Asn	
		195					200					205				
cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	agc	cat	tct	ggc	672
Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	Ser	Gly	
	210					215					220					
acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	cgc	ttc	gtg	acg	720
Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	Val	Thr	
	225				230				235					240		
gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	cgc	ggc	ttc	cgc	768
Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	Phe	Arg	
			245						250					255		
acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	atg	act	gcc	gaa	816
Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu	
			260				265						270			
gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	tcc	gtt	ctg	ccg	864
Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro	
		275				280						285				
gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	atc	agc	ttt	ggc	912
Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly	
	290				295					300						
tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	ctc	aat	tgc	cac	960
Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His	
	305				310					315				320		
cac	cac	gct	taa													972
His	His	Ala														

<210> 62  
 <211> 978  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS

<222> (1) .. (978)

<220>

<223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-truncated Shiga-A1 Subunit HIS6

<400> 62

atg ggg cca gct tct gtc cca acc acc tgc tgc ttt aac ctg gcc aat	48
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn	
1 5 10 15	
agg aag ata ccc ctt cag cga cta gag agc tac agg aga atc acc agt	96
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser	
20 25 30	
ggc aaa tgt ccc cag aaa gct gtg atc ttc aag acc aaa ctg gcc aag	144
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys	
35 40 45	
gat atc tgt gcc gac ccc aag aag aag tgg gtg cag gat tcc atg aag	192
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys	
50 55 60	
tat ctg gac caa aaa tct cca act cca aag cca gcg atg aaa gaa ttc	240
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Lys Glu Phe	
65 70 75 80	
acc ctg gac ttt tcc act gca aaa act tac gtc gat agc ctg aat gtg	288
Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val	
85 90 95	
att cgt tcc gcg atc ggt acg ccg ctg caa acg att tcc agc ggt ggt	336
Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly	
100 105 110	
act tcc ctc ctg atg att gat tcc ggt acg ggt gat aac ttg ttt gct	384
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala	
115 120 125	
gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt ttt aat aat ctg	432
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu	
130 135 140	
cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg ggt ttt gtg aac	480
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn	
145 150 155 160	
cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc tcc cac gta acg	528
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr	
165 170 175	
ttt ccg ggc acc act gct gtt act ctg agc ggc gat tct tct tat act	576
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr	
180 185 190	
acg tta cag cgt gtg gct ggt atc agc cgc act ggt atg caa atc aat	624
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn	
195 200 205	
cgc cat tct ctg acg acc agc tat ctg gac tta atg agc cat tct ggc	672
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly	
210 215 220	
acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg cgc ttc gtg acg	720
Thr Ser Leu Thr Gln Val Val Ala Arg Ala Met Leu Arg Phe Val Thr	
225 230 235 240	



gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa cgc ggc ttc cgc	768
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg	
245 250 255	
acc act tta gac gat ctg tct ggc cgc agc tat gtg atg act gcc gaa	816
Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu	
260 265 270	
gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct tcc gtt ctg ccg	864
Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro	
275 280 285	
gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt atc agc ttt ggc	912
Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly	
290 295 300	
tct att aat gcc atc cta ggc tcc gtc gca ctg att ctc aat tgc cac	960
Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His	
305 310 315 320	
cac cac cat cat cat taa	978
His His His His His	
325	

<210> 63  
 <211> 993  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(993)

<220>  
 <223> Description of Artificial Sequence: Construct encoding chemokine-toxin fusion protein EOTAXIN-AM-SAPORIN

<400> 63	
atg ggg cca gct tct gtc cca acc acc tgc tgc ttt aac ctg gcc aat	48
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn	
1 5 10 15	
agg aag ata ccc ctt cag cga cta gag agc tac agg aga atc acc agt	96
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser	
20 25 30	
ggc aaa tgt ccc cag aaa gct gtg atc ttc aag acc aaa ctg gcc aag	144
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys	
35 40 45	
gat atc tgt gcc gac ccc aag aag aag tgg gtg cag gat tcc atg aag	192
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys	
50 55 60	
tat ctg gac caa aaa tct cca act cca aag cca gcg atg gtt act agt	240
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Val Thr Ser	
65 70 75 80	
att acc ctg gac ctg gtc aat ccg acc gcc ggc caa tat agc agc ttc	288
Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe	
85 90 95	
gtg gat aag att cgt aac aac gta aaa gat ccg aat ctg aaa tac ggt	336
Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly	

100							105				110							
ggt	act	gat	att	gcg	gtc	atc	ggt	ccg	ccg	agc	aaa	gaa	aag	ttc	ctg	384		
Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	Phe	Leu			
		115					120					125						
cgc	att	aac	ttt	caa	agc	tcc	cgt	ggc	act	gtt	tct	ctg	ggc	ctg	aag	432		
Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	Leu	Lys			
	130					135					140							
cgc	gat	aac	ctg	tat	gtt	gtt	gcc	tat	ctg	gcg	atg	gat	aat	acg	aac	480		
Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	Thr	Asn			
	145				150					155					160			
gtg	aac	cgc	gcc	tac	tac	ttt	cgt	agc	gag	att	acg	agc	gcg	gaa	tcc	528		
Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr	Ser	Ala	Glu	Ser			
				165					170					175				
act	gct	ctg	ttc	ccg	gag	gcg	acc	act	gca	aac	caa	aaa	gca	ctg	gaa	576		
Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	Leu	Glu			
			180					185					190					
tat	acg	gaa	gat	tac	cag	tcc	atc	gag	aag	aac	gcg	cag	atc	acc	cag	624		
Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala	Gln	Ile	Thr	Gln			
		195					200					205						
ggc	gat	caa	tcc	cgc	aaa	gaa	ctg	ggt	ctg	ggt	att	gat	ctg	ctg	agc	672		
Gly	Asp	Gln	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile	Asp	Leu	Leu	Ser			
	210					215					220							
acg	agc	atg	gaa	gcg	gtc	aac	aaa	aaa	gct	cgc	gtg	gtt	aaa	gac	gaa	720		
Thr	Ser	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val	Val	Lys	Asp	Glu			
	225				230					235					240			
gcc	cgc	ttc	ctg	ctg	atc	gcc	att	cag	atg	acg	gca	gaa	gcc	gcc	cgt	768		
Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Ala	Ala	Arg			
				245					250					255				
ttc	cgc	tac	att	cag	aac	ctg	gtc	atc	aaa	aac	ttc	ccg	aac	aag	ttc	816		
Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	Pro	Asn	Lys	Phe			
			260					265					270					
aat	tcc	gag	aat	aaa	gtc	att	cag	ttc	gag	gtt	aat	tgg	aaa	aaa	att	864		
Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp	Lys	Lys	Ile			
		275					280					285						
tcc	acc	gcc	att	tat	ggt	gac	gcg	aag	aac	ggt	gtt	ttc	aat	aaa	gat	912		
Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	Lys	Asp			
	290					295					300							
tat	gat	ttt	ggt	ttc	ggt	aag	gta	cgt	cag	gtg	aaa	gac	ctg	caa	atg	960		
Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	Gln	Met			
	305				310					315					320			
ggt	ctg	ctg	atg	tac	cta	gga	aaa	ccg	aag	taa						993		
Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys									
				325					330									

<210> 64

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Construct encoding Methionine-truncated Shiga-A1 Subunit fusion protien

<220>

<221> CDS

<222> (1)..(744)

<400> 64

atg	aaa	gaa	ttc	acc	ctg	gac	ttt	tcc	act	gca	aaa	act	tac	gtc	gat	48
Met	Lys	Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	
1				5					10					15		
agc	ctg	aat	gtg	att	cgt	tcc	gcg	atc	ggg	acg	ccg	ctg	caa	acg	att	96
Ser	Leu	Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	
			20					25					30			
tcc	agc	ggg	ggg	act	tcc	ctc	ctg	atg	att	gat	tcc	ggg	acg	ggg	gat	144
Ser	Ser	Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	
		35					40					45				
aac	ttg	ttt	gct	gtt	gat	gtg	cgc	ggc	att	gac	ccg	gaa	gaa	ggc	cgt	192
Asn	Leu	Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	
	50					55					60					
ttt	aat	aat	ctg	cgt	ctg	atc	gtc	gaa	cgc	aac	aac	ctg	tat	gtg	acg	240
Phe	Asn	Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	
	65				70					75					80	
ggg	ttt	gtg	aac	cgt	acg	aac	aac	gtc	ttc	tat	cgt	ttc	gct	gat	ttc	288
Gly	Phe	Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	
				85					90					95		
tcc	cac	gta	acg	ttt	ccg	ggc	acc	act	gct	gtt	act	ctg	agc	ggc	gat	336
Ser	His	Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	
			100					105					110			
tct	tct	tat	act	acg	tta	cag	cgt	gtg	gct	ggg	atc	agc	cgc	act	ggg	384
Ser	Ser	Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	
		115					120					125				
atg	caa	atc	aat	cgc	cat	tct	ctg	acg	acc	agc	tat	ctg	gac	tta	atg	432
Met	Gln	Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	
	130					135					140					
agc	cat	tct	ggc	acc	agc	ctg	acc	cag	tct	gtt	gcc	cgt	gcg	atg	ctg	480
Ser	His	Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	
	145				150				155						160	
cgc	ttc	gtg	acg	gtc	acc	gcc	gaa	gcc	ctg	cgt	ttc	cgt	caa	atc	caa	528
Arg	Phe	Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	
				165					170					175		
cgc	ggc	ttc	cgc	acc	act	tta	gac	gat	ctg	tct	ggc	cgc	agc	tat	gtg	576
Arg	Gly	Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	
			180					185					190			
atg	act	gcc	gaa	gat	gtc	gat	ctg	acc	ctg	aac	tgg	ggg	cgc	ttg	tct	624
Met	Thr	Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	
		195					200					205				
tcc	gtt	ctg	ccg	gat	tat	cac	ggg	cag	gat	tct	gtc	cgt	gtt	ggc	cgt	672
Ser	Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	
	210					215					220					
atc	agc	ttt	ggc	tct	att	aat	gcc	atc	cta	ggc	tcc	gtc	gca	ctg	att	720
Ile	Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	
	225				230					235					240	
ctc	aat	tgc	cac	cac	cac	gct	taa									744
Leu	Asn	Cys	His	His	His	Ala										

<210> 65  
 <211> 750  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct encoding  
 Methionine-truncated Shiga-A1 Subunit HIS6 fusion protein

<220>  
 <221> CDS  
 <222> (1)..(750)

<400> 65  
 atg aaa gaa ttc acc ctg gac ttt tcc act gca aaa act tac gtc gat 48  
 Met Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp  
 1 5 10 15  
 agc ctg aat gtg att cgt tcc gcg atc ggt acg ccg ctg caa acg att 96  
 Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile  
 20 25 30  
 tcc agc ggt ggt act tcc ctg ctg atg att gat tcc ggt acg ggt gat 144  
 Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp  
 35 40 45  
 aac ttg ttt gct gtt gat gtg cgc ggc att gac ccg gaa gaa ggc cgt 192  
 Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg  
 50 55 60  
 ttt aat aat ctg cgt ctg atc gtc gaa cgc aac aac ctg tat gtg acg 240  
 Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr  
 65 70 75 80  
 ggt ttt gtg aac cgt acg aac aac gtc ttc tat cgt ttc gct gat ttc 288  
 Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe  
 85 90 95  
 tcc cac gta acg ttt ccg ggc acc act gct gtt act ctg agc ggc gat 336  
 Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp  
 100 105 110  
 tct tct tat act acg tta cag cgt gtg gct ggt atc agc cgc act ggt 384  
 Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly  
 115 120 125  
 atg caa atc aat cgc cat tct ctg acg acc agc tat ctg gac tta atg 432  
 Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met  
 130 135 140  
 agc cat tct ggc acc agc ctg acc cag tct gtt gcc cgt gcg atg ctg 480  
 Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu  
 145 150 155 160  
 cgc ttc gtg acg gtc acc gcc gaa gcc ctg cgt ttc cgt caa atc caa 528  
 Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln  
 165 170 175  
 cgc ggc ttc cgc acc act tta gac gat ctg tct ggc cgc agc tat gtg 576  
 Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val  
 180 185 190  
 atg act gcc gaa gat gtc gat ctg acc ctg aac tgg ggt cgc ttg tct 624  
 Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser  
 195 200 205

tcc gtt ctg ccg gat tat cac ggt cag gat tct gtc cgt gtt ggc cgt	672
Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg	
210 215 220	
atc agc ttt ggc tct att aat gcc atc cta ggc tcc gtc gca ctg att	720
Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile	
225 230 235 240	
ctc aat tgc cac cac cac cat cat cat taa	750
Leu Asn Cys His His His His His	
245 250	

<210> 66  
 <211> 765  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Construct encoding  
 Methionine-Saporin fusion protein

<220>  
 <221> CDS  
 <222> (1)..(765)

<400> 66	
atg gtt act agt att acc ctg gac ctg gtc aat ccg acc gcc ggc caa	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln	
1 5 10 15	
tat agc agc ttc gtg gat aag att cgt aac aac gta aaa gat ccg aat	96
Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn	
20 25 30	
ctg aaa tac ggt ggt act gat att gcg gtc atc ggt ccg ccg agc aaa	144
Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys	
35 40 45	
gaa aag ttc ctg cgc att aac ttt caa agc tcc cgt ggc act gtt tct	192
Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser	
50 55 60	
ctg ggc ctg aag cgc gat aac ctg tat gtt gtt gcc tat ctg gcg atg	240
Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met	
65 70 75 80	
gat aat acg aac gtg aac cgc gcc tac tac ttt cgt agc gag att acg	288
Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr	
85 90 95	
agc gcg gaa tcc act gct ctg ttc ccg gag gcg acc act gca aac caa	336
Ser Ala Glu Ser Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln	
100 105 110	
aaa gca ctg gaa tat acg gaa gat tac cag tcc atc gag aag aac gcg	384
Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala	
115 120 125	
cag atc acc cag ggc gat caa tcc cgc aaa gaa ctg ggt ctg ggt att	432
Gln Ile Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile	
130 135 140	
gat ctg ctg agc acg agc atg gaa gcg gtc aac aaa aaa gct cgc gtg	480
Asp Leu Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val	
145 150 155 160	

gtt	aaa	gac	gaa	gcc	cgc	ttc	ctg	ctg	atc	gcc	att	cag	atg	acg	gca	528
Val	Lys	Asp	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	
				165					170					175		
gaa	gcc	gcc	cgt	ttc	cgc	tac	att	cag	aac	ctg	gtc	atc	aaa	aac	ttc	576
Glu	Ala	Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	
			180					185					190			
ccg	aac	aag	ttc	aat	tcc	gag	aat	aaa	gtc	att	cag	ttc	gag	gtt	aat	624
Pro	Asn	Lys	Phe	Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	
		195					200					205				
tgg	aaa	aaa	att	tcc	acc	gcc	att	tat	ggg	gac	gcg	aag	aac	ggg	gtt	672
Trp	Lys	Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	
	210					215					220					
ttc	aat	aaa	gat	tat	gat	ttt	ggg	ttc	ggg	aag	gta	cgt	cag	gtg	aaa	720
Phe	Asn	Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	
	225				230					235				240		
gac	ctg	caa	atg	ggg	ctg	ctg	atg	tac	cta	gga	aaa	ccg	aag	taa		765
Asp	Leu	Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys			
				245					250					255		

<210> 67  
 <211> 231  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)..(231)

<220>  
 <223> Description of Artificial Sequence: Construct encoding Methionine-MCP3 protein

<400> 67																
atg	caa	ccg	gta	ggc	atc	aac	acg	tcg	acc	acg	tgc	tgt	tat	cgc	ttt	48
Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	
1				5					10					15		
atc	aac	aag	aaa	atc	ccg	aaa	caa	cgc	ctg	gaa	tcc	tat	cgt	cgc	acc	96
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	
			20					25					30			
act	agc	agc	cac	tgt	ccg	cgc	gaa	gca	gtc	atc	ttc	aaa	acc	aag	ctc	144
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	
			35				40					45				
gat	aag	gaa	atc	tgt	gca	gac	ccg	act	cag	aaa	tgg	gtg	caa	gat	ttt	192
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	
	50					55					60					
atg	aaa	cat	ctg	gat	aag	aaa	act	cag	acc	ccg	aag	ctt				231
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu				
	65				70					75						

<210> 68  
 <211> 4  
 <212> PRT  
 <213> Pseudomonas aeruginosa

<220>  
 <221> MOD\_RES

```

<222> (1)
<223> Lys or Arg

<220>
<221> REPEAT
<222> (1)...(4)
<223> repeat unit 1-6 times

<220>
<223> Pseudomonas toxin carboxy-terminal endoplasmic reticulum retention
signal

<400> 68
Xaa Asp Glu Leu
1

<210> 69
<211> 393
<212> DNA
<213> Mus musculus

<220>
<223> Mouse chemokine ALP cDNA

<220>
<221> CDS
<222> (11)..(373)

<400> 69
ctgagtgagc atg atg gag ggg ctc tcc ccc gcc agc agc ctc ccg ctg      49
          Met Met Glu Gly Leu Ser Pro Ala Ser Ser Leu Pro Leu
              1              5              10

tta ctg ttg ctt ctg agc ccg gct cct gaa gca gcc ttg cct ctg ccc      97
Leu Leu Leu Leu Leu Ser Pro Ala Pro Glu Ala Ala Leu Pro Leu Pro
    15              20              25

tcc agc act agc tgc tgt act cag ctc tat aga cag cca ctc cca agc      145
Ser Ser Thr Ser Cys Cys Thr Gln Leu Tyr Arg Gln Pro Leu Pro Ser
    30              35              40              45

agg ctg ctg agg agg att gtc cac atg gaa ctg cag gag gcc gat ggg      193
Arg Leu Leu Arg Arg Ile Val His Met Glu Leu Gln Glu Ala Asp Gly
              50              55              60

gac tgt cac ctc cag gct gtc gtg ctt cac ctg gct cgg cgc agt gtc      241
Asp Cys His Leu Gln Ala Val Val Leu His Leu Ala Arg Arg Ser Val
              65              70              75

tgt gtt cat ccc cag aac cgc agc ctg gct cgg tgg tta gaa cgc caa      289
Cys Val His Pro Gln Asn Arg Ser Leu Ala Arg Trp Leu Glu Arg Gln
    80              85              90

ggg aaa agg ctc caa ggg act gta ccc agt tta aat ctg gta cta caa      337
Gly Lys Arg Leu Gln Gly Thr Val Pro Ser Leu Asn Leu Val Leu Gln
    95              100              105

aag aaa atg tac tca aac ccc caa cag caa aac taa taaagcaaca      383
Lys Lys Met Tyr Ser Asn Pro Gln Gln Gln Asn
    110              115              120

ttagacgaca      393

<210> 70
<211> 912
<212> DNA

```

<213> Mus musculus

<220>

<223> Mouse Lungkine cDNA

<220>

<221> CDS

<222> (1)..(504)

<300>

<308> AF082859/GenBank

<400> 70

atg gct gct caa ggc tgg tcc atg ctc ctg ctg gct gtc ctt aac cta	48
Met Ala Ala Gln Gly Trp Ser Met Leu Leu Leu Ala Val Leu Asn Leu	
1 5 10 15	

ggc atc ttc gtc cgt ccc tgt gac act caa gag cta cga tgt ctg tgt	96
Gly Ile Phe Val Arg Pro Cys Asp Thr Gln Glu Leu Arg Cys Leu Cys	
20 25 30	

att cag gaa cac tct gaa ttc att cct ctc aaa ctc att aaa aat ata	144
Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile Lys Asn Ile	
35 40 45	

atg gtg ata ttc gag acc att tac tgc aac aga aag gaa gtg ata gca	192
Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys Glu Val Ile Ala	
50 55 60	

gtc cca aaa aat ggg agt atg att tgt ttg gat cct gat gct cca tgg	240
Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp Pro Asp Ala Pro Trp	
65 70 75 80	

gtg aag gct act gtt ggc cca att act aac agg ttc cta cct gag gac	288
Val Lys Ala Thr Val Gly Pro Ile Thr Asn Arg Phe Leu Pro Glu Asp	
85 90 95	

ctc aaa caa aag gaa ttt cca ccg gca atg aag ctt ctg tat agt gtt	336
Leu Lys Gln Lys Glu Phe Pro Pro Ala Met Lys Leu Leu Tyr Ser Val	
100 105 110	

gag cat gaa aag cct cta tat ctt tca ttt ggg aga cct gag aac aag	384
Glu His Glu Lys Pro Leu Tyr Leu Ser Phe Gly Arg Pro Glu Asn Lys	
115 120 125	

aga ata ttt ccc ttt cca att cgg gag acc tct aga cac ttt gct gat	432
Arg Ile Phe Pro Phe Pro Ile Arg Glu Thr Ser Arg His Phe Ala Asp	
130 135 140	

tta gct cac aac agt gat agg aat ttt cta cgg gac tcc agt gaa gtc	480
Leu Ala His Asn Ser Asp Arg Asn Phe Leu Arg Asp Ser Ser Glu Val	
145 150 155 160	

agc ttg aca ggc agt gat gcc taa aagccactca tgaggcaaag agtttcaagg	534
Ser Leu Thr Gly Ser Asp Ala	
165	

aagctctcct cctggagttt tggcgttctc attcttatac tctattcccg cgttagtctg 594

gtgtatggat ctatgagctc tcttttaata ttttattata aatgttttat ttacttaact 654

tcttagtgaa tgttcacagg tgactgctcc cccatcccca tttcttgata ttacatataa 714

tgggcatcata tacccttcta ttgactgaca aactactcag attgcttaac attttgtgct 774

tcaaagtcctt atcccactcc actatgggct gttacagagt gcatctcggg gtagagcaag 834



gctccttgtc ttcagtgccc caggggtgaaa tactttctttg aaaaattttc attcatcaga 894  
 raatctgaaa taaatatt 912

<210> 71  
 <211> 325  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
 MCP1-AM-truncated Shiga-A1 Subunit

<400> 71  
 Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe  
 1 5 10 15  
 Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile  
 20 25 30  
 Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val  
 35 40 45  
 Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser  
 50 55 60  
 Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys  
 65 70 75 80  
 Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu  
 85 90 95  
 Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser  
 100 105 110  
 Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu  
 115 120 125  
 Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn  
 130 135 140  
 Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe  
 145 150 155 160  
 Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His  
 165 170 175  
 Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser  
 180 185 190  
 Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln  
 195 200 205  
 Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His  
 210 215 220  
 Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe  
 225 230 235 240  
 Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly  
 245 250 255  
 Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr  
 260 265 270  
 Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val  
 275 280 285  
 Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser  
 290 295 300  
 Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn  
 305 310 315 320  
 Cys His His His Ala  
 325

<210> 72  
 <211> 327  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
 MCP1-AM-truncated Shiga-A1 Subunit HIS6

```

<400> 72
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
 1          5          10          15
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
          20          25          30
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
          35          40          45
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
 50          55          60
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Lys
 65          70          75          80
Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu
          85          90          95
Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser
          100          105          110
Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu
          115          120          125
Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn
          130          135          140
Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe
          145          150          155          160
Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His
          165          170          175
Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser
          180          185          190
Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln
          195          200          205
Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His
          210          215          220
Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe
          225          230          235          240
Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly
          245          250          255
Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr
          260          265          270
Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val
          275          280          285
Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser
          290          295          300
Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn
          305          310          315          320
Cys His His His His His His
          325

```

```

<210> 73
<211> 332
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Chemokine-toxin fusion protein
MCP1-AM-SAPORIN

```

```

<400> 73
Met Gln Pro Asp Ala Ile Asn Ala Pro Val Thr Cys Cys Tyr Asn Phe
 1          5          10          15
Thr Asn Arg Lys Ile Ser Val Gln Arg Leu Ala Ser Tyr Arg Arg Ile
          20          25          30
Thr Ser Ser Lys Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Ile Val
          35          40          45
Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln Lys Trp Val Gln Asp Ser
 50          55          60
Met Asp His Leu Asp Lys Gln Thr Gln Thr Pro Lys Thr Ala Met Val

```

65	Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	80
					85					90						95	
	Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	
				100				105						110			
	Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	
			115					120					125				
	Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	
		130					135					140					
	Leu	Lys	Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	
145					150						155					160	
	Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr	Ser	Ala	
				165						170					175		
	Glu	Ser	Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	
			180						185					190			
	Leu	Glu	Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala	Gln	Ile	
		195						200					205				
	Thr	Gln	Gly	Asp	Gln	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile	Asp	Leu	
		210				215						220					
	Leu	Ser	Thr	Ser	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val	Val	Lys	
225					230						235					240	
	Asp	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Ala	
				245						250					255		
	Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe	Pro	Asn	
			260					265					270				
	Lys	Phe	Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn	Trp	Lys	
		275					280						285				
	Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	
		290				295					300						
	Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	
305					310						315					320	
	Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys					
				325					330								

<210> 74

<211> 325

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
MCP3-AM-truncated Shiga-A1 Subunit

<400> 74

Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe	
1				5					10					15		
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr	
			20					25					30			
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	
		35					40					45				
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe	
	50					55					60					
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu	Ala	Met	Lys	
	65				70				75					80		
Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	
			85						90					95		
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	
			100				105						110			
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	
		115					120					125				
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	
	130					135					140					
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	
145					150					155					160	
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	

Val	Thr	Phe	Pro	165	Thr	Thr	Ala	Val	170	Thr	Leu	Ser	Gly	175	Asp	Ser	Ser
			180	Gly					185					190			
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln		
		195					200						205				
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His		
	210					215					220						
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe		
225					230					235					240		
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly		
				245					250					255			
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr		
			260					265					270				
Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val		
		275					280						285				
Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser		
	290					295					300						
Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn		
305				310					315						320		
Cys	His	His	His	Ala													
				325													

<210> 75

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
MCP3-AM-truncated Shiga-A1 subunit HIS6

<400> 75

Met	Gln	Pro	Val	Gly	Ile	Asn	Thr	Ser	Thr	Thr	Cys	Cys	Tyr	Arg	Phe		
1				5					10					15			
Ile	Asn	Lys	Lys	Ile	Pro	Lys	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Thr		
		20					25						30				
Thr	Ser	Ser	His	Cys	Pro	Arg	Glu	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu		
		35				40						45					
Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Thr	Gln	Lys	Trp	Val	Gln	Asp	Phe		
	50					55				60							
Met	Lys	His	Leu	Asp	Lys	Lys	Thr	Gln	Thr	Pro	Lys	Leu	Ala	Met	Lys		
65				70					75					80			
Glu	Phe	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu		
			85					90					95				
Asn	Val	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser		
			100				105						110				
Gly	Gly	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu		
		115					120					125					
Phe	Ala	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn		
	130					135					140						
Asn	Leu	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe		
145				150					155					160			
Val	Asn	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His		
			165				170						175				
Val	Thr	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser		
		180					185						190				
Tyr	Thr	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln		
		195				200						205					
Ile	Asn	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His		
	210					215					220						
Ser	Gly	Thr	Ser	Leu	Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe		
225				230						235					240		
Val	Thr	Val	Thr	Ala	Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly		
				245					250					255			
Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr		



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemokine-toxin fusion protein SDF-1-Beta-AM-truncated Shiga-A1 Subunit

<400> 77

```
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1          5          10          15
His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
          20          25          30
Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
          35          40          45

Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 50          55          60

Ala Leu Asn Lys Arg Phe Lys Met Ala Met Lys Glu Phe Thr Leu Asp
 65          70          75          80
Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser
          85          90          95
Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly Thr Ser Leu
          100          105          110
Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala Val Asp Val
          115          120          125
Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile
          130          135          140
Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn
          145          150          155          160
Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly
          165          170          175
Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln
          180          185          190
Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser
          195          200          205
Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu
          210          215          220
Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala
          225          230          235          240
Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu
          245          250          255
Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp
          260          265          270
Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro Asp Tyr His
          275          280          285
Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn
          290          295          300
Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His His His Ala
          305          310          315          320
```

<210> 78

<211> 322

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemokine-toxin fusion protein SDF-1-Beta-AM-truncated Shiga-A1 Subunit HIS6

<400> 78

```
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 1          5          10          15
```

His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr	Pro
			20					25					30		
Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg	Gln
		35					40					45			
Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu	Lys
	50					55					60				
Ala	Leu	Asn	Lys	Arg	Phe	Lys	Met	Ala	Met	Lys	Glu	Phe	Thr	Leu	Asp
	65				70					75					80
Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn	Val	Ile	Arg	Ser
			85						90					95	
Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly	Gly	Thr	Ser	Leu
			100					105					110		
Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	Phe	Ala	Val	Asp	Val
		115					120					125			
Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn	Leu	Arg	Leu	Ile
	130					135						140			
Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val	Asn	Arg	Thr	Asn
	145				150					155					160
Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His	Val	Thr	Phe	Pro	Gly
			165						170					175	
Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr	Thr	Thr	Leu	Gln
			180					185					190		
Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	Ile	Asn	Arg	His	Ser
		195					200					205			
Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	Ser	Gly	Thr	Ser	Leu
	210					215						220			
Thr	Gln	Ser	Val	Ala	Arg	Ala	Met	Leu	Arg	Phe	Val	Thr	Val	Thr	Ala
	225				230					235					240
Glu	Ala	Leu	Arg	Phe	Arg	Gln	Ile	Gln	Arg	Gly	Phe	Arg	Thr	Thr	Leu
			245						250					255	
Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val	Met	Thr	Ala	Glu	Asp	Val	Asp
		260						265					270		
Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser	Ser	Val	Leu	Pro	Asp	Tyr	His
		275					280					285			
Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg	Ile	Ser	Phe	Gly	Ser	Ile	Asn
	290					295					300				
Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile	Leu	Asn	Cys	His	His	His	His
	305				310					315					320
His	His														

<210> 79  
 <211> 327  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Chemokine-toxin fusion protein SDF-1-Beta-AM-SAPORIN

<400>	79														
Lys	Pro	Val	Ser	Leu	Ser	Tyr	Arg	Cys	Pro	Cys	Arg	Phe	Phe	Glu	Ser
	1			5					10					15	
His	Val	Ala	Arg	Ala	Asn	Val	Lys	His	Leu	Lys	Ile	Leu	Asn	Thr	Pro
		20						25					30		
Asn	Cys	Ala	Leu	Gln	Ile	Val	Ala	Arg	Leu	Lys	Asn	Asn	Asn	Arg	Gln
		35					40					45			
Val	Cys	Ile	Asp	Pro	Lys	Leu	Lys	Trp	Ile	Gln	Glu	Tyr	Leu	Glu	Lys
	50					55					60				
Ala	Leu	Asn	Lys	Arg	Phe	Lys	Met	Ala	Met	Val	Thr	Ser	Ile	Thr	Leu
	65				70					75					80
Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	Ser	Phe	Val	Asp	Lys
			85					90						95	
Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	Tyr	Gly	Gly	Thr	Asp
		100						105					110		
Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	Phe	Leu	Arg	Ile	Asn

Phe	Gln	115	Ser	Ser	Arg	Gly	Thr	120	Val	Ser	Leu	Gly	Leu	125	Lys	Arg	Asp	Asn
130	Leu	Tyr	Val	Val	Ala	Tyr	Leu	135	Ala	Met	Asp	Asn	Thr	140	Asn	Val	Asn	Arg
145	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	150	Ile	Thr	Ser	Ala	Glu	155	Ser	Thr	Ala	Leu
160	Phe	Pro	Glu	Ala	Thr	Thr	Ala	165	Asn	Gln	Lys	Ala	Leu	170	Glu	Tyr	Thr	Glu
175	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	180	Asn	Ala	Gln	Ile	Thr	185	Gln	Gly	Asp	Gln
190	Ser	Arg	Lys	Glu	Leu	Gly	Leu	195	Gly	Ile	Asp	Leu	Leu	200	Ser	Thr	Ser	Met
205	Glu	Ala	Val	Asn	Lys	Lys	Ala	210	Arg	Val	Val	Lys	Asp	215	Glu	Ala	Arg	Phe
220	225	Leu	Leu	Ile	Ala	Ile	Gln	230	Met	Thr	Ala	Glu	Ala	235	Ala	Arg	Phe	Arg
240	Ile	Gln	Asn	Leu	Val	Ile	Lys	245	Asn	Phe	Pro	Asn	Lys	250	Phe	Asn	Ser	Glu
255	Asn	Lys	Val	Ile	Gln	Phe	Glu	260	Val	Asn	Trp	Lys	Lys	265	Ile	Ser	Thr	Ala
270	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	275	Gly	Val	Phe	Asn	Lys	280	Asp	Tyr	Asp	Phe
285	Gly	Phe	Gly	Lys	Val	Arg	Gln	290	Val	Lys	Asp	Leu	Gln	295	Met	Gly	Leu	Leu
300	305	Met	Tyr	Leu	Gly	Lys	Pro	310	Lys					315				320
325																		

<210> 80

<211> 323

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
EOTAXIN-AM-truncated Shiga-A1 Subunit

<400> 80

Met	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys	Cys	Phe	Asn	Leu	Ala	Asn
1	Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser	Tyr	Arg	Arg	Ile	Thr
5	Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe	Lys	Thr	Lys	Leu	Ala
10	Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Trp	Val	Gln	Asp	Ser	Met	Lys
15	Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys	Pro	Ala	Met	Lys	Glu
20	Thr	Leu	Asp	Phe	Ser	Thr	Ala	Lys	Thr	Tyr	Val	Asp	Ser	Leu	Asn
25	Ile	Arg	Ser	Ala	Ile	Gly	Thr	Pro	Leu	Gln	Thr	Ile	Ser	Ser	Gly
30	Thr	Ser	Leu	Leu	Met	Ile	Asp	Ser	Gly	Thr	Gly	Asp	Asn	Leu	Phe
35	Val	Asp	Val	Arg	Gly	Ile	Asp	Pro	Glu	Glu	Gly	Arg	Phe	Asn	Asn
40	Arg	Leu	Ile	Val	Glu	Arg	Asn	Asn	Leu	Tyr	Val	Thr	Gly	Phe	Val
45	145	Arg	Thr	Asn	Asn	Val	Phe	Tyr	Arg	Phe	Ala	Asp	Phe	Ser	His
50	Phe	Pro	Gly	Thr	Thr	Ala	Val	Thr	Leu	Ser	Gly	Asp	Ser	Ser	Tyr
55	Thr	Leu	Gln	Arg	Val	Ala	Gly	Ile	Ser	Arg	Thr	Gly	Met	Gln	Ile
60	Arg	His	Ser	Leu	Thr	Thr	Ser	Tyr	Leu	Asp	Leu	Met	Ser	His	Ser
65															
70															
75															
80															
85															
90															
95															
100															
105															
110															
115															
120															
125															
130															
135															
140															
145															
150															
155															
160															
165															
170															
175															
180															
185															
190															
195															
200															
205															
210															
215															
220															
225															
230															
235															
240															
245															
250															
255															
260															
265															
270															
275															
280															
285															
290															
295															
300															
305															
310															
315															
320															
325															



210	215	220
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr		
225	230	235
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg		240
	245	250
Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu		255
	260	265
Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro		270
	275	280
Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly		285
	290	295
Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His		300
305	310	315
His His Ala		320

<210> 81  
 <211> 325  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
 EOTAXIN-AM-truncated Shiga-A1 Subunit HIS6

<400> 81

Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn	
1 5 10 15	
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser	
20 25 30	
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys	
35 40 45	
Asp Ile Cys Ala Asp Pro Lys Lys Trp Val Gln Asp Ser Met Lys	
50 55 60	
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Lys Glu Phe	
65 70 75 80	
Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp Ser Leu Asn Val	
85 90 95	
Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile Ser Ser Gly Gly	
100 105 110	
Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp Asn Leu Phe Ala	
115 120 125	
Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg Phe Asn Asn Leu	
130 135 140	
Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr Gly Phe Val Asn	
145 150 155 160	
Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe Ser His Val Thr	
165 170 175	
Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp Ser Ser Tyr Thr	
180 185 190	
Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly Met Gln Ile Asn	
195 200 205	
Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met Ser His Ser Gly	
210 215 220	
Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu Arg Phe Val Thr	
225 230 235 240	
Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln Arg Gly Phe Arg	
245 250 255	
Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val Met Thr Ala Glu	
260 265 270	
Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser Ser Val Leu Pro	
275 280 285	
Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg Ile Ser Phe Gly	
290 295 300	
Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile Leu Asn Cys His	
305 310 315 320	

His His His His His  
325

<210> 82  
<211> 330  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Chemokine-toxin fusion protein  
EOTAXIN-AM-SAPORIN

<400> 82  
Met Gly Pro Ala Ser Val Pro Thr Thr Cys Cys Phe Asn Leu Ala Asn  
1 5 10 15  
Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr Arg Arg Ile Thr Ser  
20 25 30  
Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys Thr Lys Leu Ala Lys  
35 40 45  
Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val Gln Asp Ser Met Lys  
50 55 60  
Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro Ala Met Val Thr Ser  
65 70 75 80  
Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe  
85 90 95  
Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly  
100 105 110  
Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu  
115 120 125  
Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys  
130 135 140  
Arg Asp Asn Leu Tyr Val Ala Tyr Leu Ala Met Asp Asn Thr Asn  
145 150 155 160  
Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala Glu Ser  
165 170 175  
Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu  
180 185 190  
Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln  
195 200 205  
Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Ser  
210 215 220  
Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asp Glu  
225 230 235 240  
Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala Ala Arg  
245 250 255  
Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn Lys Phe  
260 265 270  
Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys Lys Ile  
275 280 285  
Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp  
290 295 300  
Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met  
305 310 315 320  
Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys  
325 330

<210> 83  
<211> 247  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Methionine-truncated Shiga-A1  
Subunit fusion protein

<400> 83  
Met Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp  
1 5 10 15  
Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile  
20 25 30  
Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp  
35 40 45  
Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg  
50 55 60  
Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr  
65 70 75 80  
Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe  
85 90 95  
Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp  
100 105 110  
Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly  
115 120 125  
Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met  
130 135 140  
Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu  
145 150 155 160  
Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln  
165 170 175  
Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser Tyr Val  
180 185 190  
Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg Leu Ser  
195 200 205  
Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val Gly Arg  
210 215 220  
Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala Leu Ile  
225 230 235 240  
Leu Asn Cys His His His Ala  
245

<210> 84  
<211> 249  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Methionine-truncated Shiga-A1  
Subunit HIS6 fusion protein

<400> 84  
Met Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr Val Asp  
1 5 10 15  
Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Pro Leu Gln Thr Ile  
20 25 30  
Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Thr Gly Asp  
35 40 45  
Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Pro Glu Glu Gly Arg  
50 55 60  
Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr Val Thr  
65 70 75 80  
Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala Asp Phe  
85 90 95  
Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser Gly Asp  
100 105 110  
Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg Thr Gly  
115 120 125  
Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp Leu Met  
130 135 140  
Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala Met Leu  
145 150 155 160  
Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Phe Arg Gln Ile Gln

				165					170					175			
Arg	Gly	Phe	Arg	Thr	Thr	Leu	Asp	Asp	Leu	Ser	Gly	Arg	Ser	Tyr	Val		
			180					185					190				
Met	Thr	Ala	Glu	Asp	Val	Asp	Leu	Thr	Leu	Asn	Trp	Gly	Arg	Leu	Ser		
		195					200					205					
Ser	Val	Leu	Pro	Asp	Tyr	His	Gly	Gln	Asp	Ser	Val	Arg	Val	Gly	Arg		
	210					215					220						
Ile	Ser	Phe	Gly	Ser	Ile	Asn	Ala	Ile	Leu	Gly	Ser	Val	Ala	Leu	Ile		
225					230					235					240		
Leu	Asn	Cys	His	His	His	His	His	His									
				245													

<210> 85  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Methionine-Saporin fusion protein

<400>	85																
Met	Val	Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln		
1				5					10					15			
Tyr	Ser	Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn		
			20					25					30				
Leu	Lys	Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys		
		35					40					45					
Glu	Lys	Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser		
	50					55					60						
Leu	Gly	Leu	Lys	Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met		
65					70				75						80		
Asp	Asn	Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr		
			85						90					95			
Ser	Ala	Glu	Ser	Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln		
		100						105					110				
Lys	Ala	Leu	Glu	Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala		
	115						120					125					
Gln	Ile	Thr	Gln	Gly	Asp	Gln	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile		
	130					135						140					
Asp	Leu	Leu	Ser	Thr	Ser	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val		
145					150					155					160		
Val	Lys	Asp	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala		
			165						170					175			
Glu	Ala	Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Ile	Lys	Asn	Phe		
		180						185					190				
Pro	Asn	Lys	Phe	Asn	Ser	Glu	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Asn		
	195					200					205						
Trp	Lys	Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val		
	210					215					220						
Phe	Asn	Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys		
225					230					235					240		
Asp	Leu	Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys				
			245						250								

<210> 86  
 <211> 77  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Methionine-MCP3 fusion protein

<400> 86  
 Met Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe  
           1                  5                  10                  15  
 Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr  
                   20                  25                  30  
 Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu  
                   35                  40                  45  
 Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe  
           50                  55                  60  
 Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu  
           65                  70                  75

<210> 87  
 <211> 120  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> Mouse chemokine ALP

<400> 87  
 Met Met Glu Gly Leu Ser Pro Ala Ser Ser Leu Pro Leu Leu Leu Leu  
           1                  5                  10                  15  
 Leu Leu Ser Pro Ala Pro Glu Ala Ala Leu Pro Leu Pro Ser Ser Thr  
                   20                  25                  30  
 Ser Cys Cys Thr Gln Leu Tyr Arg Gln Pro Leu Pro Ser Arg Leu Leu  
                   35                  40                  45  
 Arg Arg Ile Val His Met Glu Leu Gln Glu Ala Asp Gly Asp Cys His  
           50                  55                  60  
 Leu Gln Ala Val Val Leu His Leu Ala Arg Arg Ser Val Cys Val His  
           65                  70                  75                  80  
 Pro Gln Asn Arg Ser Leu Ala Arg Trp Leu Glu Arg Gln Gly Lys Arg  
                   85                  90  
 Leu Gln Gly Thr Val Pro Ser Leu Asn Leu Val Leu Gln Lys Lys Met  
                   100                  105                  110  
 Tyr Ser Asn Pro Gln Gln Gln Asn  
           115                  120

<210> 88  
 <211> 167  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> Mouse Lungkine

<400> 88  
 Met Ala Ala Gln Gly Trp Ser Met Leu Leu Leu Ala Val Leu Asn Leu  
           1                  5                  10                  15  
 Gly Ile Phe Val Arg Pro Cys Asp Thr Gln Glu Leu Arg Cys Leu Cys  
                   20                  25                  30  
 Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile Lys Asn Ile  
                   35                  40                  45  
 Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys Glu Val Ile Ala  
           50                  55                  60  
 Val Pro Lys Asn Gly Ser Met Ile Cys Leu Asp Pro Asp Ala Pro Trp  
           65                  70                  75                  80  
 Val Lys Ala Thr Val Gly Pro Ile Thr Asn Arg Phe Leu Pro Glu Asp  
                   85                  90                  95  
 Leu Lys Gln Lys Glu Phe Pro Pro Ala Met Lys Leu Leu Tyr Ser Val  
                   100                  105                  110  
 Glu His Glu Lys Pro Leu Tyr Leu Ser Phe Gly Arg Pro Glu Asn Lys

Arg	Ile	115	Phe	Pro	Phe	Pro	Ile	120	Arg	Glu	Thr	Ser	Arg	125	His	Phe	Ala	Asp
	130						135						140					
Leu	Ala	His	Asn	Ser	Asp	Arg	Asn	Phe	Leu	Arg	Asp	Ser	Ser	Glu	Val			
145					150					155					160			
Ser	Leu	Thr	Gly	Ser	Asp	Ala												
				165														

<210> 89  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Human Chemokine polypeptide: NAP-2  
 <300>  
 <301> Clark-Lewis et. al.,  
 <303> J. Leukoc. Biol.  
 <304> 57  
 <306> 703-711  
 <307> 1995  
 <400> 89

Ala	Glu	Leu	Arg	Cys	Met	Cys	Ile	Lys	Thr	Thr	Ser	Gly	Ile	His	Pro
1				5					10					15	
Lys	Asn	Ile	Gln	Ser	Leu	Glu	Val	Ile	Gly	Lys	Gly	Thr	His	Cys	Asn
			20					25					30		
Gln	Val	Glu	Val	Ile	Ala	Thr	Leu	Lys	Asp	Gly	Arg	Lys	Ile	Cys	Leu
		35					40					45			
Asp	Pro	Asp	Ala	Pro	Arg	Ile	Lys	Lys	Ile	Val	Gln	Lys	Lys	Leu	Ala
	50					55					60				
Gly	Asp	Glu	Ser	Ala	Asp										
65					70										

<210> 90  
 <211> 78  
 <212> PRT  
 <213> Homo sapiens  
 <220>  
 <223> Human Chemokine Polypeptide: ENA-78

<300>  
 <301> Clark-Lewis et. al.,  
 <303> J. Leukoc. Biol.  
 <304> 57  
 <306> 703-711  
 <307> 1995

Ala	Gly	Pro	Ala	Ala	Ala	Val	Leu	Arg	Glu	Leu	Arg	Cys	Val	Cys	Leu
1				5					10					15	
Gln	Thr	Thr	Gln	Gly	Val	His	Pro	Lys	Met	Ile	Ser	Asn	Leu	Gln	Val
			20					25					30		
Phe	Ala	Ile	Gly	Pro	Gln	Cys	Ser	Lys	Val	Glu	Val	Val	Ala	Ser	Leu
		35					40					45			
Lys	Asn	Gly	Lys	Glu	Ile	Cys	Leu	Asp	Pro	Glu	Ala	Pro	Phe	Leu	Lys
	50					55				60					
Lys	Val	Ile	Gln	Lys	Ile	Leu	Asp	Gly	Gly	Asn	Lys	Glu	Asn		
65					70					75					

<210> 91  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<220>  
<223> Human Chemokine polypeptide: PF-4

<300>  
<301> Clark-Lewis et. al.,  
<303> J. Leukoc. Biol.  
<304> 57  
<306> 703-711  
<307> 1995

<400> 91  
Glu Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr  
1 5 10 15  
Ser Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala  
20 25 30  
Gly Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly  
35 40 45  
Arg Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile  
50 55 60  
Lys Lys Leu Leu Glu Ser  
65 70

<210> 92  
<211> 74  
<212> PRT  
<213> Homo sapiens  
<220>  
<223> Human Chemokine Polypeptide: gamma-IP-10

<300>  
<301> Clark-Lewis et. al.,  
<303> J. Leukoc. Biol.  
<304> 57  
<306> 703-711  
<307> 1995

<400> 92  
Ser Arg Thr Val Arg Cys Thr Cys Ile Ser Ile Ser Asn Gln Pro Val  
1 5 10 15  
Asn Pro Arg Ser Leu Glu Lys Leu Glu Ile Ile Pro Ala Ser Gln Phe  
20 25 30  
Cys Pro Arg Val Glu Ile Ile Ala Thr Met Lys Lys Lys Gly Glu Lys  
35 40 45  
Arg Cys Leu Asn Pro Glu Ser Lys Ala Ile Lys Asn Leu Leu Lys Ala  
50 55 60  
Val Ser Lys Glu Met Ser Lys Arg Ser Pro  
65 70

<210> 93  
<211> 93  
<212> PRT  
<213> Homo sapiens  
<220>  
<223> Human Chemokine Polypeptide: Stromal cell-derived  
Factor-1-Beta (SDF-1-Beta)

<300>  
<303> Genomics  
<304> 28  
<306> 495-500

<307> 1995

<400> 93

Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
1 5 10 15  
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
20 25 30  
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
35 40 45  
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
50 55 60  
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
65 70 75 80  
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
85 90